

GenCore version 5.1.3  
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OM nucleic - nucleic search, using SW model

Run on: October 11, 2002, 02:43:44 : Search time 3214 Seconds  
(without alignments)  
11277.150 Million cell updates/sec

Title: US-09-530-233-1  
Perfect score: 1732  
Sequence: 1 tgcacagcagcggtcttgcgc.....tgcatacaaaaaaaaaa

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vl:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*  
29: em.vl:\*  
30: em.htg.hum:\*  
31: em.htg.in:\*  
32: em.htg.other:\*  
33: em.htg.in:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Query Score Match Length DB ID Description

Result No.	Query	Score	Match Length	DB	ID	Description
1	1732	100.0	1732	6	A97008	A97008 Sequence 1
2	1732	100.0	1732	6	AX286634	AX286634 Sequence
3	1732	100.0	1732	6	AF057711	AF057711 Homo sapi
4	1717.2	99.1	1746	9	AF095897	AF095897 Homo sapi
5	1715.2	99.0	1736	6	AR168531	AR168531 Sequence
6	1653.6	95.5	1736	9	AB010575	AB010575 Homo sapi
7	1588.8	91.7	1650	6	A82597	A82597 Sequence 5
8	1588.8	91.7	1650	6	AF195025	AF195025 Homo sapi
9	1583.8	91.4	1723	6	A82593	A82593 Sequence 1
10	1551.8	89.6	1632	9	AF195024	AF195024 Homo sapi
11	1508.2	87.1	1711	6	A82595	A82595 Sequence 3
12	1508.2	87.1	1711	6	A82786	A82786 Sequence 1
13	1096.4	63.3	1602	6	A87685	A87685 Sequence 5
14	1096.4	63.3	1602	6	AR168529	AR168529 Sequence
15	1086.4	63.3	1602	6	AX286638	AX286638 Sequence
16	1096.4	63.3	1602	10	AF01358	AF013588 Rattus no
17	538	31.1	216408	2	AC092466	AC092466 Homo sapi
18	538	31.1	222605	9	AC010973	AC010973 Homo sapi
19	536.4	31.0	213045	2	AC093640	AC093640 Homo sapi
20	472.2	27.3	2962	6	A98491	A98491 Sequence 1
21	472.2	27.3	2962	10	RN06519	AJ006519 Rattus no
22	470.6	27.2	3449	10	RN030926	AJ309926 Rattus no
23	470.6	27.2	3647	6	A87684	A87684 Sequence 4
24	470.6	27.2	3647	6	AR168528	AR168528 Sequence
25	466.8	27.0	3785	9	HSU78181	U78181 Human sodiu
26	456.8	26.4	1620	6	A87682	AR16862 Sequence 2
27	456.8	26.4	1620	6	AR168526	AR168526 Sequence
28	453.2	26.2	3488	10	RN094403	U94403 Rattus norv
29	453.2	26.2	3562	6	A87681	AR16861 Sequence 1
30	453.2	26.2	3562	6	AR168525	AR168525 Sequence
31	423.2	24.4	2711	6	AX002412	AX002412 Sequence
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33	420.6	24.3	1632	6	AX002418	AX002418 Sequence
34	420.6	24.3	1632	6	E31846	E31846 Novel compo
35	416.2	24.0	1663	9	HSU53212	U53212 Human degen
36	416.2	24.0	1666	6	AR16863	AR16863 Sequence 3
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## ALIGNMENTS

RESULT 1  
A97008 LOCUS A97008 1732 bp DNA linear PAT 26-JAN-2000  
DEFINITION Sequence 1 from Patent WO9921981.  
ACCESSION A97008  
VERSION A97008.1 GI:6780449  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified.  
unclassified.  
REFERENCE 1 (bases 1 to 1732)  
Babinski, K. and Seguela, P.  
DNA ENCODING A HUMAN PROTON-GATED ION CHANNEL AND USES THEREOF  
Patent: WO 9921981-A 1 06-MAY-1999;  
JOURNAL UNIV MCGILL (CA); BABINSKI KAZIMIERZ (CA)  
FEATURES  
source  
1. 1732  
/organism="unidentified"  
/db\_xref="taxon:32644"  
22. 1617  
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/db\_xref="GI:6780450"  
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BASE COUNT 326 a 601 c 484 g 321 t  
ORIGIN

Query Match 100.0%; Score 1732; DB 6; Length 1732;  
Best Local Similarity 100.0%; Pred. No. 2,1e-288;  
Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
AX286634 1732 bp DNA linear PAT 21-NOV-2001  
LOCUS  
DEFINITION Sequence 3 from Patent W00181570.  
ACCESSION AX286634  
VERSION AX286634.1 GI:17048709  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (sites)  
 AUTHORS Seguela, P. and Babin, K.  
 TITLE Heteromultimeric ion channel receptor and uses thereof  
 JOURNAL Patent: WO 0181570-A 3 01-NOV-2001;  
 MCGILL UNIVERSITY (CA)  
 FEATURES  
 source location/Qualifiers  
 1. 1732  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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BASE COUNT 326 a 601 c 484 g 321 t

ORIGIN

Query Match 100.0%; Score 1732; DB 6; Length 1732;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-288;  
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 Db 181 GCCACCTTCTACAGAGTGGGAGAGGGTGGCTACTACAGAGGATTCACACAG 240

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 Db 1441 AACGAG 1500

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 Db 1501 CATGAG 1560

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 Db 1561 GTACAG 1620

QY 1621 TGT 1680  
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 Db 1621 TGT 1680

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 Db 1681 CTTTTCGCTTCAACCCCAATTAAGTCTTAATGATCAAAAAA 1732

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 LOCUS 1732 bp mRNA linear PRI 06-OCT-1998  
 DEFINITION Homo sapiens proton-gated cation channel subunit (ASIC3) mRNA,  
 complete cds.  
 ACCESSION AF057711  
 VERSION AF057711.1 GI:3702835  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
		(bases 1 to 1732)					
	Babinski, K., Le, K.-T. and Seguela, P.	Cloning, functional properties and distribution of a non-desensitizing proton-gated channel from human brain unpublished					
		2 (bases 1 to 1732)					
	Babinski, K., Le, K.-T. and Seguela, P.	Direct Submission					
		Submitted (06-APR-1998)					
	Neurology & Neurosurgery, Montreal Neurological Institute, 3801 University, Montreal, QC H3A 2B4, Canada						
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		/dev_stage="fetus"					
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		/gene="ASIC3"					
		22..1617					
		/gene="ASIC3"					
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	Best Local Similarity	100.0%	Pred. No. 2.1e-288;				
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Db	421	GCACGCCCCGGCTTCATGCCACAGTCCACCTTTGACATGGCGCAACTCTATGCCCCGT	480
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Db	481	GGGCACTCCCTGGATGACATGCTGCGACGTGCTTCCGTGGCCAACTTGTGGGCT	540
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Qy	601	GATGGGGCAGAGCTGCTACCACTACTAGGGGGTGGCATGGGCAATGGGCTGGACATATG	660
Db	601	GATGGGGCAGAGCTGCTACCACTACTAGGGGGTGGCATGGGCAATGGGCTGGACATATG	660
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Qy	781	GGCTTGGGGGTGTCGCCGGCTACACAGACTTTGTTCTTCTGCGACGACGACGTGAGC	840
Db	781	GGCTTGGGGGTGTCGCCGGCTACACAGACTTTGTTCTTCTGCGACGACGACGTGAGC	840
Qy	841	TTTCTGCGACCGCCCTGGGGGATTTGAGATTCAAGCATCTGTGAAACCCCAACTATGAGCA	900
Db	841	TTTCTGCGACCGCCCTGGGGGATTTGAGATTCAAGCATCTGTGAAACCCCAACTATGAGCA	900
Qy	901	GAGCCCTTGATGCCCTTAGGCTCCCCAGCGCCCAAGCCCAAGCCCTTCTATACCCCTATG	960
Db	901	GAGCCCTTGATGCCCTTAGGCTCCCCAGCGCCCAAGCCCAAGCCCTTCTATACCCCTATG	960
Qy	961	GAGGTGCGCTGGCTGCGAAACCCGCTACGTGCTGCGAATGGCGCTGCCGAATGGTG	1020
Db	961	GAGGTGCGCTGGCTGCGAAACCCGCTACGTGCTGCGAATGGCGCTGCCGAATGGTG	1020
Qy	1021	TACATGCCAGCGACGAGCCAGTGTGAGCGCCCGACAGATGACAAAGATGTGCCACCG	1080
Db	1021	TACATGCCAGCGACGAGCCAGTGTGAGCGCCCGACAGATGACAAAGATGTGCCACCG	1080
Qy	1081	GCCATGATGCCATCTTTCGAAAGACTGTGCGCTGCCCCCAACCGTGGCGCAGACG	1140
Db	1081	GCCATGATGCCATCTTTCGAAAGACTGTGCGCTGCCCCCAACCGTGGCGCAGACG	1140
Qy	1141	CGCTACGCGCAAGGAGCTCTCATGTGCGGATCCGAGCGCGCGCGCGGGGCTTCGTG	1200
Db	1141	CGCTACGCGCAAGGAGCTCTCATGTGCGGATCCGAGCGCGCGCGCGGGGCTTCGTG	1200
Qy	1201	GCCCGGAAGCTCAACCGCAGCGACTACATGCGGAGAACGTGTGCGCTCTGGACATC	1260
Db	1201	GCCCGGAAGCTCAACCGCAGCGACTACATGCGGAGAACGTGTGCGCTCTGGACATC	1260
Qy	1261	TTTCTTGAAGGCCCTCACTATGAGACCGTGGACACAAAGAGGCCCTATGATGTGCAGG	1320
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Qy	1321	CTGCTTGGTGCATTTGGGGGCGAGATGGGCTTTTATCGGGGCGACGCTGTGCACATC	1380
Db	1321	CTGCTTGGTGCATTTGGGGGCGAGATGGGCTTTTATCGGGGCGACGCTGTGCACATC	1380
Qy	1381	CTCGAGATCTAGACTACCTCTGTGAGGTTCGAGACAAAGTCTCTGGGATATTTCTGG	1440
Db	1381	CTCGAGATCTAGACTACCTCTGTGAGGTTCGAGACAAAGTCTCTGGGATATTTCTGG	1440
Qy	1441	AACCGACGACCTCCCAAAGGCACTCCAGACCAATCTGTTDAGGAAGGCTGGGCAAC	1500
Db	1441	AACCGACGACCTCCCAAAGGCACTCCAGACCAATCTGTTDAGGAAGGCTGGGCAAC	1500
Qy	1501	CATGAACCCCAAGTTCCCACTCAGCTTGGGCCCAAGACTTCCACCCCTCCCTGTAGC	1560



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Db 1621 TGTGCTGTGCTGCTGAGAGCCCGCCCTGACATCTGAGCATGCTAGCTAG 1680  
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RESULT 4  
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LOCUS Homo sapiens proton-gated cation channel ASIC3 mRNA, complete cds.  
DEFINITION AF095897  
ACCESSION AF095897.1 GI:3747100  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1746)  
de Weille,J.R., Bassilana,F., Lazdunski,M. and Waldmann,R.  
TITLE Identification, functional expression and chromosomal localisation  
of a sustained human proton-gated cation channel  
JOURNAL FEBS Lett. 433 (3), 257-260 (1998)  
MEDLINE 98416055  
REFERENCE 2 (bases 1 to 1746)  
de Weille,J.R., Bassilana,F., Lazdunski,M. and Waldmann,R.  
AUTHORS Direct Submission  
TITLE Submitted (28-SEP-1998) IPMC, CNRS, University of Nice/Sophia  
JOURNAL Antipolis, 660 Route des Lucioles, 06560 Valbonne 06560, France  
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/translation="MKPTSGPEARRPASDIRVFASNCSMHGLGHVFGSLSRGM  
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LIDCRREGQPCRPENTTITFTMGKCYTNSGADGELLITTRTGKNSLIDLDVQ  
EEYLPRWNEETPEVGIKQVHISQEEPIIDQLGLVSPQVTSQOQDLFLP  
PWWGSSASLNENPEPSDPLSGSPSPYLTMGRLCETVYVARKCCRAVY  
MGDVPVCSPOQKNCAPALDAMLRKDCACPNPCASRYRAKELMSPSAARF  
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BASE COUNT 338 a 598 c 489 g 321 t  
ORIGIN

Query Match 99.1%; Score 1717.2; DB 9; Length 1746;  
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QY 123 GCCAGGACGCTGAGCCCTGCGCCGGGGGATGTGGAGCGCGCGGTGCTCTGACAGGC 182  
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QY 843 CTTGCGACCGCCCTGGGGCGATTGTCAGTCTGATGACATCTGTAACCCCAACTATGAGCCAGA 902  
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QY 1143 CTACGCCAAGAGAGCTTCATGTTGGCGGATCCGAGCGCGCGCGCTTCTGCG 1202  
Db 1149 CTACGCCAAGAGAGCTTCATGTTGGCGGATCCGAGCGCGCGCGCTTCTGCG 1208  
QY 1203 CCGGAAGCTCAACCGCAGCGAGGCTTACATCGGCGGAAGATGTGCTGCGCTGGACATCTT 1262

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Db 1209 CCGAAGCTCAACCGAGGAGCCCTACATCGGAGAACGTGCTGGCCCTGGACATCTT 1268  
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ABI68531 1736 bp DNA linear PAT 17-DEC-2001  
LOCUS DEFINITION Sequence 13 from patent US 6287859.  
ACCESSION AR168531  
VERSION AR168531.1 GI:17904498  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1736)  
AUTHORS DeMille,J.R., Bassilana,F., Lazdunski,M. and Rahner,W.  
TITLE Identification, functional expression and chromosomal localization of  
a sustained human Proton-gated cation channel  
JOURNAL Patent: US 6287859-A 13 11-SEP-2001;  
FEATURES  
source 1..1736  
BASE COUNT 335 a 596 c 486 g 319 t  
ORIGIN

Query Match 99.0%; Score 1715.2; DB 6; Length 1736;  
Best Local Similarity 99.5%; Pred. No.1.6e-285;  
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 ACCESSION AB010575  
 VERSION AB010575.1 GI:3097313  
 KEYWORDS DRASIC; sodium channel.  
 SOURCE Homo sapiens male testis cDNA to mRNA.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Ishibashi, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JAN-1998) Kenichi Ishibashi, Tokyo Medical and Dental University, 2nd Internal Medicine; yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: kishibashi.med2@med.tmd.ac.jp, Tel: 81-3-5803-5223, Fax: 81-3-5803-0132)  
 REFERENCE 2 (sites)

REFERENCE  
 AUTHORS Ishibashi, K. and Marumo, F.  
 TITLE Molecular cloning of a DEG/ENaC sodium channel cDNA from human testis  
 JOURNAL Biochem. Res. Commun. 245 (2), 589-593 (1998)  
 MEDLINE 98238685  
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CDS

polya\_site  
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 Db 802 GCTGCTCACACACTCTAGGGGTGGGATGGGCAATGGGCTGGGCACTCAATGGGCGAGTGA 861  
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Db	1222	AGCGCAGCTGCCAGTGTGTCAGCCGCCAGCATCAAGAATCTGTGCCACCCGGCCATAGA	1281
QY	1089	TGCATCTCTTCGCAAGGACTTCGGGCGCTGCCCAACCCGTGGCGGACGACGGCGTATAGC	1148
Db	1282	TGCATCTCTTCGCAAGGACTTCGGGCGCTGCCCAACCCGTGGCGGACGACGGCGTATAGC	1341
QY	1149	CAAGAGCTCTCCATGTGTGCGGATCCCGAGCCGCGCGCGCGCGCTTCGTGGCCCGGAA	1208
Db	1342	CAAGAGCTCTCCATGTGTGCGGATCCCGAGCCGCGCGCGCGCGCTTCGTGGCCCGGAA	1401
QY	1209	GCTCAACCGCCAGAGGCGCTACATGGCGGAGAACTGTGTGCGCTGTGGACATCTTCTTTGA	1268
Db	1402	GTTCAACCGCCAGAGGCGCTACATGGCGGAGAACTGTGTGCGCTGTGGACATCTTCTTTGA	1461
QY	1269	GGCCCTCAACTATGAGACCCGTGGAGCAGAAAGGCGCTTGTGAGATGTACAGCTGCTTGG	1328
Db	1462	GGCCCTCAACTATGAGACCCGTGGAGCAGAAAGGCGCTTGTGAGATGTACAGCTGCTTGG	1521
QY	1329	TGACATTTGGGGGCCAGATGGGCCCTTTTCAATCGGGGCCAGCTGTCTACCATCTCGAGAT	1388
Db	1522	TGACATTTGGGGGCCAGATGGGGCTGTTTATCGGGGCCAGCTGTCTACCATCTCGAGAT	1581
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QY	1449	GCACATCCCAAGAGCACTCCAGCACCACATCTGTTAGAGAAAGGCTGTGGCAGCATCGAAC	1508
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QY	1509	CCAAGTTGCCCACTCAGCTGTGGGGCCCAAGACCTCCACCCCTCCCTGTGGCGTACCAA	1568
Db	1702	CCAAATTTCCCACTCAGCTGTGGGGCCCAAGACCTCCACCCCTCCCTGTGGCGTACCAA	1761
QY	1569	GACCTCTCCGCGCTCCACACCGGACCTGTGACCTTGTGACACAGCTCTAGACCTGTGCT	1628
Db	1762	GACCTTTTCCGCGCTCCACACCGGACCTGTGACCTTGTGACACAGCTCTAGACCTGTGCT	1821
QY	1629	GTGTCTCTGGAGCCCGCGCTGTACATCTGTGACATGCTTAGCTAGCTCAGCTATTTTCG	1688
Db	1822	GTGTCTCTGGAGCCCGCGCTGTACATCTGTGACATGCTTAGCTAGCTCAGCTATTTTCG	1881
QY	1689	TCTTACCCCAATTAAGTCTTAATGCAATC 1718	
Db	1882	TCTTACCCCAATTAAGTCTTAATGCAATC 1911	

RESULT 7	
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LOCUS	AB2597 1650 bp DNA
DEFINITION	Sequence 5 from Patent WO9854316.
ACCESSION	AB2597
VERSION	AB2597.1 GI:6732341
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1650)
AUTHORS	Graham,D. and Renard,S.
TITLE	SODIUM CHANNEL RECEPTOR
JOURNAL	Patent: WO 9854316-A 5 03-DEC-1998;

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Query Match		91.7%	Score 1588.8	DB 6	Length 1650
Best Local Similarity		98.4%	Pred. No. 8.9e-264		
Matches 1623	Conservative	0	Mismatches	7	Indels
				20	Gaps
					1
OY	22	ATGAAGCCCACTCAGGCGCCAGAGAGAGGCCCGGGCGGACGCCCTCGGACATCCGGCTTTC	81		
Db	1	ATGAAGCCCACTCAGGCGCCAGAGAGAGGCCCGGGCGGACGCCCTCGGACATCCGGCTTTC	60		
OY	82	GCCACACACTGCTGCATGCACGGGCTGGGGCCACGCTCTGGGGCCAGAGAGCTAGGCTG	141		
Db	61	GCCACACACTGCTGCATGCACGGGCTGGGGCCACGCTCTGGGGCCAGAGAGCTAGGCTG	120		
OY	142	CGCCCGGGGGATGTGGGCGAGCGGCCGTGTCTCTGTCACTAGTGGCCACCTTCTTACAGAGTG	201		
Db	121	CGCCGGGGGATGTGGGCGAGCGGCCGTGTCTCTGTCACTAGTGGCCACCTTCTTACAGAGTG	180		
OY	202	GCTGAGAGGGTGGCGCTACTACAGAGGAGTTCCACCACCAAGATGCCCTGGATGAGCGAGAA	261		
Db	181	GCTGAGAGGGTGGCGCTACTACAGAGGAGTTCCACCACCAAGATGCCCTGGATGAGCGAGAA	240		
OY	262	AGCCACCGGCTCGTCTCCGGCTGTCACTCTGTGCAATCAACCCACTCGCGCGTGC	321		
Db	241	AGCCACCGGCTCGTCTCCGGCTGTCTCCGGCTGTCACTCTGTGCAATCAACCCACTCGCGCGTGC	300		
OY	322	CGCCTAACGCCCAACGACCTGCACCTGGGCTGGGTGCGCTGTGGGCTTGATCCCGCA	381		
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OY	382	GAGCAGCGCGGCTTCCTCCGCGGCCCTGGGGCGGGCCCTCGACCGCCGGCTTATGCC	441		
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Db	421	AGTCACACCTTTGACATGGCGCAACTCTATGCCCCGTGTGGGCACTCCCTGGATGACATG	480		
OY	502	CTGCTGGACTGTGCTTCCGTTCGGTGCCCAACCTTGTGGGCTGAGAACTTACACAGATTTTC	561		
Db	481	CTGCTGGACTGTGCTTCCGTTCGGTGCCCAACCTTGTGGGCTGAGAACTTACACAGATTTTC	540		
OY	562	ACCCGGATGGGAAAGTGTATACATTTTAACCTGTGCGCTGATGGGGGAGAGGCTCTACC	621		
Db	541	ACCCGGATGGGAAAGTGTATACATTTTAACCTGTGCGCTGATGGGGGAGAGGCTCTACC	600		
OY	622	ACTACTAGGGGTGGCATGGGCAATGGGCTGGACATCATGCTGACGCTGACGACAGAGAA	681		
Db	601	ACTACTAGGGGTGGCATGGGCAATGGGCTGGACATCATGCTGACGCTGACGACAGAGAA	660		

QY	682	TATCTACCTGTGTGGAGGACAAATGAGAGACCCGTTTGAGGTGGGATCCGATGCAG	741
DB	661		
QY	742	ATCCACAGCAGGAGAGAGCCGCATCATCATGATCAGCTGGGCTTGGGGGTGTCCCGGGC	801
DB	721		
QY	802	TACCAAGACCTTGTCTTCCAGCAGCAGCAGTGAAGTTCTTCCGACCGCCCTGGGGC	861
DB	781		
QY	862	GATTGAGTTCAGATCTGTGAACCCCACTATGAGCCAGAGCCCTGTATCCCTAGGC	921
DB	841		
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DB	901		
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DB	961		
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DB	1021		
QY	1102	AAGGACTGTGGGCGCTGCCCAACCCGCTGCGCAGCAGCGGCTAGCCCAAGAGCTCTCC	1161
DB	1081		
QY	1162	ATGTTGCGGATCCCGAGCCGCGCGCGCGCTCTTCTGCGCGGAAGCTCAACCGCAGC	1221
DB	1141		
QY	1222	GAGGCTACATGGCGGAGAAAGTGTGCGCTTGGACATCTTCTTGAAGCCCTCAACTAT	1281
DB	1201		
QY	1282	GAGACCGTGGAGAGAAAGGCGTATGATGTAGAGCTGCTGTGATTTGGGGGC	1341
DB	1261		
QY	1342	CAGATGGGCTTTTCAATGGGGCCAGCGCTCAGCATCTCTCGAGATCTTAGACTCTTC	1401
DB	1321		
QY	1402	TGTGAGGTGTCCGAGACAAAGGCTCGGAGATTTCTGGAACCGAGCACTCCCAAAG	1461
DB	1381		
QY	1462	CACCTCAGACCAATCTGCTTCAAGAAAGGCTGGGAGCCATTCGAACCAAGTTCCCAAC	1521
DB	1441		
QY	1522	CTCAGGCTGGGGCC-----AGACCTCCCAACCCCTCCCTGTGGCG	1561
DB	1501		
QY	1562	TCACCAAGACTCTTCGGGCTCCACGAGCAGTACCTTGTGACACAGCTTAAAGCT	1621
DB	1561		
QY	1622	GCTGTCTGTCTCTGGAGCCCGGCGCTGA	1651
DB	1621		

RESULT 8  
AF195025  
LOCUS AF195025 1650 bp mRNA linear PRI 26-DEC-1999

DEFINITION	Homo sapiens acid sensing ion channel 3 splice variant c mRNA, complete cds.	
ACCESSION	AF195025	
VERSION	AF195025.1 GI:6635434	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Renard,S., Besnard,F., Partiseti,M. and Graham,D.	
TITLE	ASIC3c a new member of the acid sensing ion channel family	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1650)	
AUTHORS	Renard,S., Besnard,F., Partiseti,M. and Graham,D.	
TITLE	Direct Submission	
JOURNAL	Submitted (14-Oct-1999) Functional Genomics, Sanofi-Synthelabo, 10 rue des carrieres, Rueil Malmaison 92500, France	
FEATURES	location/Qualifiers	
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Best Local Similarity	98.4%; Pred. No. 8.9e-264;	
Matches 1623; Conservative	0; Mismatches 7; Indels 20; Gaps 1;	
QY	22 ATGAAGCCCACTCAGAGCCCGAGAGAGGCCGCGGCGAGCCCTCGACATCCGCTGTTCC	81
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QY	82 GCCAGCACTGCTCGATGACAGCGGCTGGGCGACGCTCTGGGCGCAGGCAAGCCGAGCCTG	141
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QY	142 CGCGGGGAGATGTGGGCGAGCGGCGGTGCTCTCAAGTGCGCACTTCTCTACAGAGT	201
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QY	202 GCTGAAGGGTGGCTACTACAGAGGAGTTCCACACCAAGCTGCTCGATGAGCGAGAA	261
DB	181 GCTGAAGGGTGGCTACTACAGAGGAGTTCCACACCAAGCTGCTCGATGAGCGAGAA	240
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DB	241 AGCCACCGGCTGCTCTTCCCGGCTGTACACCTGTGCAACATCAACCAAGCCGCGCTCG	300
QY	322 CGCCTAAGCGCCAAAGCACTGCACTGGGCTGGGTGTGCGCTGTGGGCTGATATCCCGCA	381
DB	301 CGCCTAAGCGCCAAAGCACTGCACTGGGCTGGGTGTGCGCTGTGGGCTGATATCCCGCA	360
QY	382 GAGCAGCGCGCTTCTCTGCGCGCCCTGGGCGGCGCCCTGACCGCGCGCTTATATGCC	441
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RESULT 9
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DEFINITION Sequence 1 from Patent WO9854316.
ACCESSION AB2593
VERSION AB2593.1 GI:6732338
KEYWORDS
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ORGANISM human.
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1723)
AUTHORS Graham,D. and Renard,S.
TITLE SODIUM CHANNEL RECEPTOR
JOURNAL Patent: WO 9854316-A 1 03-DEC-1998;
GRAHAM DAVID (FR); RENARD STEPHANE (FR)
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ORIGIN

Query Match 91.4%; Score 1583.8; DB 6; Length 1723;
Best Local Similarity 96.2%; Pred. No. 6.4e-263;
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OY 70 ATCCGCGTTCGCGCAGCAACTGCTGATGACAGGCGCTGGGCCAGCTTTCGGGCCAGGC 129
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DEFINITION	AF195024	Homo sapiens acid sensing ion channel 3 splice variant b mRNA,	
ACCESSION	AF195024	complete cds.	
VERSION	AF195024.1	GI:6635432	
KEYWORDS		human.	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE		1 (bases 1 to 1632)	
AUTHORS		Renard,S., Besnard,F., Partiseti,M. and Graham,D.	
TITLE		AS1C3b a new modulatory subunit of the acid sensing ion channel family	
JOURNAL		unpublished	
REFERENCE		2 (bases 1 to 1632)	
AUTHORS		Renard,S., Besnard,F., Partiseti,M. and Graham,D.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-Oct-1999) Functional Genomics, Sanofi-Synthelabo, 10	
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 VERSION A82595.1 GI:6732340  
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 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1711)  
 AUTHORS Graham,D. and Renard,S.  
 TITLE SODIUM CHANNEL RECEPTOR  
 JOURNAL Patent: WO 9854316-A 3 03-DEC-1998;  
 GRAHAM DAVID (FR); RENARD STEPHANE (FR)  
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VERSION	AB2786.1	GI:6732465										
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SOURCE	human.											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.											
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JOURNAL	Graham,D. and Renard,S.											
FEATURES	Sodium channel receptor											
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Query Match 87.1%; Score 1508.2; DB 6; Length 1711;  
Best Local Similarity 95.9%; Pred. No. 6,5e-250;  
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DEFINITION Sequence 5 from Patent WO9835034.

ACCESSION AB7685

VERSION AB7685.1 GI:6736306

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 1602)

AUTHORS Heurteaux, C. and Champigny, G.

TITLE MAMMAL NEURONAL ACID SENSING CATIONIC CHANNEL, CLONING AND

# APPLICATIONS THEREOF Patent: WO 9835034-A 5 13-AUG-1998:

JOURNAL  
HEURTEAUX CATHERINE (FR); CHAMIGNY GUY (FR)  
FEATURES  
Location/Qualifiers

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LOCUS ARI68529  
DEFINITION Sequence 9 from patent US 6287859.  
ACCESSION ARI68529  
VERSION ARI68529.1 GI:17904495  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1602)  
AUTHORS DeWelle, J.R., Bassiliana, F., Lazdunski, M. and Rainer, W.  
TITLE Identification, functional expression and chromosomal localization of a sustained human proton-gated cation channel  
JOURNAL Patent: US 6287859-A 9 11-SEP-2001;  
FEATURES Location/Qualifiers  
source 1. .1602  
/organism="unknown"  
BASE COUNT 328 a 498 c 434 g 342 t  
ORIGIN

Query Match 63.3%; Score 1096.4; DB 6; Length 1602;  
Best Local Similarity 81.2%; Pred. No. 4.3e-179;

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Db	25	GAGGCGGCGGCGGAGCCCTGGACATCCGCGTGTCCGCGAGCAAGCTCGATGAC	84	
Oy	103	GGGCGGCGGAGCTTGGGCGGAGGAGCCCTGAGCCCTGGGCGGAGTGGGCGAGC	162	
Db	85	GCTGTGGGCGACATCTTGGCCCTGGAGGCGCTGACCTGGCGCGGAGGGGTGGGCGACA	144	
Oy	163	GCCGTGGCTGTCTAGTGGCCACTTCCCTCTACAGTGGCTGAGAGGGGTGGGCTACTAC	222	
Db	145	GCTGTGGCTGTCTAGTGGCCACTTCCCTCTACAGTGGCTGAGAGGGGTGGGCTACTAT	204	
Oy	223	AGGGAGTTCACACACAGACTGCGCTGTGATGAGCAGAGAAAGCCAGCGGCTCTTCCCG	282	
Db	205	GGGGAGTTCACACATAGACACACCTGTGATGAGCTGAGAGCCAGCAGCTTCCCA	264	
Oy	283	GCTGTACCCCTGTGCAACATCAACCCACTGCGCGCTGCGGCTTAAGGCCAAGAGACTG	342	
Db	265	GCTGTACTGTGTATATCAACCCACTGCGCGCTCAAGCCCTCAACCCAAATGACTTG	324	
Oy	343	CACGTGGGCTGTGGGCTGTGGGCTGTGGATCCCGCAGAGACAGCCGCTTCTCGGC	402	
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Oy	823	CAGCAGCAGCAGCTGAGCTTCTGTGACCGCCCTGTGGGCGATGTGAGATCTCTTG	882	
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Db	865	GATCCCGAGCTTGTATTCAGAGCCCTGTATCCCTTGTGGTTCGCCAGCCAGAC	924	
Oy	940	AGCCCTCCCTTATACCTTATGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	999	
Db	925	AGCCCTCCCTTATAGTTTAAATAGTTGTGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	984	
Oy	1000	AAGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	1059	
Db	985	AAGTGTGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	1044	
Oy	1060	TACAAGAACTGTGGCGACCGGCGCTTATAGTGCATCTTCCGAGAGACTGTGGGCTGTG	1119	
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Db	1285	GGCGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	1344	
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LOCUS AX286638  
DEFINITION Sequence 7 from Patent W00181570.  
ACCESSION AX286638  
VERSION AX286638.1 GI:17048711  
KEYWORDS  
SOURCE  
ORGANISM  
Rattus sp.  
Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
1 (sites)  
AUTHORS Seguela P. and Bablinski K.  
TITLE Heteromultimeric ion channel receptor and uses thereof  
JOURNAL Patent: WO 0181570-A 7 01-NOV-2001;  
MCgILL UNIVERSITY (CA)  
LOCATION/Qualifiers  
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BASE COUNT 328 a 498 c 434 g 342 t  
ORIGIN  
Query Match 63.3%; Score 1096.4; DB 6; Length 1602;  
Best Local Similarity 81.2%; Pred. NO. 4.3e-179;  
Matches 1282: Conservative 0: Mismatches 293: Indels 3: Gaps 1:

Oy	43	GAGGAGGCGCGGCGGAGCCCTGGACATCCGCGTGTCCGCGAGCAAGCTCGATGAC	102	
Db	25	GAGGCGGCGGCGGAGCCCTGGACATCCGCGTGTCCGCGAGCAAGCTCGATGAC	84	
Oy	103	GGGCGGCGGAGCTTGGGCGGAGGAGCCCTGAGCCCTGGGCGGAGTGGGCGAGC	162	
Db	85	GCTGTGGGCGACATCTTGGCCCTGGAGGCGCTGACCTGGCGCGGAGGGGTGGGCGACA	144	
Oy	163	GCCGTGGCTGTCTAGTGGCCACTTCCCTCTACAGTGGCTGAGAGGGGTGGGCTACTAC	222	
Db	145	GCTGTGGCTGTCTAGTGGCCACTTCCCTCTACAGTGGCTGAGAGGGGTGGGCTACTAT	204	
Oy	223	AGGGAGTTCACACACAGACTGCGCTGTGATGAGCAGAGAAAGCCAGCGGCTCTTCCCG	282	
Db	205	GGGGAGTTCACACATAGACACACCTGTGATGAGCTGAGAGCCAGCAGCTTCCCA	264	
Oy	283	GCTGTACCCCTGTGCAACATCAACCCACTGCGCGCTGCGGCTTAAGGCCAAGAGACTG	342	
Db	265	GCTGTACTGTGTATATCAACCCACTGCGCGCTCAAGCCCTCAACCCAAATGACTTG	324	
Oy	343	CACGTGGGCTGTGGGCTGTGGGCTGTGGATCCCGCAGAGACAGCCGCTTCTCGGC	402	
Db	325	CACGTGGGCTGTGAACAGCGCTGTGGGCTGTGAGCCTGTGAACATGTGCTTCTCGT	384	
Oy	403	GCCCTGGGCGGCGGCGGCTGACCGCGGCTTCATGCCAGTCCCACTTTGACATGGCG	462	
Db	385	GCACGTGGGCGGCGGCGGCGGCTTGTGATGCCAGTCCGACCTTTGACATGGCA	444	
Oy	463	CACCTCTATGCCCGCTGTGGGCGGCTGTGGATGACATGTGCTGTGAGCTGTGCTCGT	522	
Db	445	CAACCTCTATGCCCGGAGGCGGCGGCTGTGGATGACATGTGCTGTGAGCTGTGCTCGT	504	
Oy	523	GCCCAACCTGTGGGCTGTGAGAACTTCAACAGATCTTACCCGGATGGGAAAGTGTAC	582	
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Db	565	ACCTTCAATCTGTGTGGGCGGAGGCTGTGAGGCTGTCTACCACTACTAGGGGTGGATGGGC	624	
Oy	643	AATGGGCTGTGACATGTGTGTGACGTGACGACGAGAGAAATCTACTGTGTGAGAGGAC	702	
Db	625	AACGACTGTGAGATGTCTAGATGTACAGCAAGAGAGATCTCCCATCTGGAAAGAC	684	
Oy	703	AATGAGGAGACCCGTTTGGAGGTGGGATCCGAGTGCAGATCCACAGCAGAGAGAGCG	762	
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Db	805	CAGCAGCAGCAGCTGAGCTTCTGTGACCGCCCTGTGGGCGATGTGAGATCTCTTG	864	
Oy	883	AAACCCACTA--TGACCGCAGAGCCCTGTATCCCTTACAGCTTCCCGCAGCCCGCC	939	
Db	865	GATCCCGAGCTTGTATTCAGAGCCCTGTATCCCTTGTGGTTCGCCAGCCAGAC	924	
Oy	940	AGCCCTCCCTTATACCTTATGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	999	
Db	925	AGCCCTCCCTTATAGTTTAAATAGTTGTGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	984	
Oy	1000	AAGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	1059	
Db	985	AAGTGTGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG	1044	
Oy	1060	TACAAGAACTGTGGCGACCGGCGCTTATAGTGCATCTTCCGAGAGACTGTGGGCTGTG	1119	
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Search completed: October 11, 2002, 03:45:58  
 Job time : 3225 secs





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 02:43:14 ; Search time 284 Seconds

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	1583.8	91.4	1723	20	AAV84189
6	1508.2	87.1	1711	20	AAV84190
7	1096.4	63.3	1602	19	AAV60843
8	1096.4	63.3	1602	21	AA561201
9	1096.4	63.3	1602	24	AA561201

10	472.2	27.3	2962	20	AA5628161
11	470.6	27.2	3647	19	AAV60842
12	470.6	27.2	3647	21	AA561200
13	456.8	26.4	1620	19	AAV60840
14	456.8	26.4	1620	21	AA561198
15	453.2	26.2	3562	19	AAV60839
16	453.2	26.2	3562	21	AA561197
17	423.2	24.4	2711	19	AAV68056
18	421	24.3	2528	22	AA561265
19	420.6	24.3	1632	19	AAV68059
20	416.2	24.0	1666	19	AAV60841
21	416.2	24.0	1666	21	AA561199
22	416.2	24.0	2565	24	AA561127
23	415.8	24.0	1539	20	AA5623167
24	415.8	24.0	2748	24	AA5617125
25	391.4	22.6	2622	21	AA563802
26	352.2	20.3	1948	19	AAV60844
27	352.2	20.3	1948	21	AA561202
28	288.6	16.7	2955	19	AAV68057
29	246.8	14.2	1203	21	AA563924
30	246.8	14.2	2516	21	AA563923
31	191	11.0	192	20	AA5617133
32	174	10.0	960	20	AA5628162
33	170.4	9.8	451	22	ABA13241
34	170.4	9.8	451	22	AA162780
35	165.2	9.5	508	19	AAV68058
36	148.8	8.6	152	24	AA5617137
37	99	5.7	354	22	AAH35552
38	91.6	5.3	444	22	AAK31936
39	87.8	5.1	271	22	AA137802
40	87.8	5.1	271	22	ABA70302
41	87.8	5.1	271	22	AAK18532
42	87.8	5.1	271	22	AAK44449
43	87.8	5.1	271	22	AA150442
44	78.2	4.5	490	22	ABA57682
45	78.2	4.5	490	22	AAK05740

#### ALIGNMENTS

RESULT 1	AA56237	standard; DNA; 1732 Bp.
ID	AA56237	
AC	AA56237	
XX		
DT	16-JUL-1999	(first entry)
XX		
DE	Human proton-gated cation channel encoding DNA.	
XX		
KW	Human; non-inactivating amiloride-sensitive proton-gated cation channel;	
KW	hASIC3; analgesic; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	key	Location/Qualifiers
FT	CDS	22..1617
FT		/*tag- a
XX		
PN	W09921981-A1.	
XX		
PD	06-MAY-1999.	
XX		
PF	29-OCT-1998;	98WO-CA01016.
XX		
PR	29-OCT-1997;	97CA-2219713.
XX		
PA	(UYMC-) UNITV MCGILL.	
XX		
PI	Babinski K, Seguela P;	
XX		
DR	WPI; 1999-312958/26.	

Rat Acid sensitive  
Rat acid sensing i  
cDNA encoding a ra  
Partial human acid  
cDNA encoding a pa  
Rat acid sensing i  
cDNA encoding a ra  
Neurodegenerative  
Human brain sodium  
Neurodegenerative  
Human acid sensing  
cDNA encoding a hu  
Rat cDNA encoding  
Human BNC1 cDNA..  
Human cDNA encodin  
Nucleic acid encod  
Rat acid sensing i  
cDNA encoding a ra  
Neurodegenerative  
Coding region of a  
DNA encoding a hum  
Human cDNA encodin  
Rat Acid sensitive  
Human nervous syst  
Human cDNA SEQ ID  
Neurodegenerative  
Human cDNA encodin  
Human colon cancer  
Human bone marrow  
Probe #6488 used t  
Human brain expres  
Human bone marrow  
Probe #19128 used  
Human foetal liver  
Human brain expres

DR P-PSDB; AA09509.

XX Use of human protein as a proton-gated cation channel

XX Claim 1; Fig 1; 32pp; English.

XX The present sequence encodes a human non-inactivating amiloride-sensitive  
CC proton-gated cation channel designated hASIC3. hASIC3, its encoding  
CC nucleic acid and the recombinant host cell are useful in a composition  
CC or a kit for screening compounds useful as proton-gated cation channel  
CC ligands. The ligands are useful as analgesics.

XX Sequence 1732 BP; 326 A; 601 C; 484 G; 321 T; 0 other;

Query Match 100.0%; Score 1732; DB 20; Length 1732;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 TCGCAGCAGCGGGTCTGGCATGAAGCCACCTCAGGCCAGAGAGGCCGGGGCAG 60
DB 1 TCGCAGCAGCGGGTCTGGCATGAAGCCACCTCAGGCCAGAGAGGCCGGGGCAG 60
OY 61 CCCCTGGACATCCGGCTGTCTCCAGCAACTCTGATGCAGGGCTGGGCCACTTTC 120
DB 61 CCCCTGGACATCCGGCTGTCTCCAGCAACTCTGATGCAGGGCTGGGCCACTTTC 120
OY 121 GGGCCAGCAGCCTGAGCTGCGCGGGGATGTGGGAGCGCGGCTGTCTCAGTG 180
DB 121 GGGCCAGCAGCCTGAGCTGCGCGGGGATGTGGGAGCGCGGCTGTCTCAGTG 180
OY 181 GCCACCTTCTTACCAAGGTGCTGAGAGGGTGCCTACTACAGGAGTTCCACACAG 240
DB 181 GCCACCTTCTTACCAAGGTGCTGAGAGGGTGCCTACTACAGGAGTTCCACACAG 240
OY 241 ACTGCCCTGGATGAGCGAAGAACCGGGCTGCTCCGGGCTGACACCTGTGCAAC 300
DB 241 ACTGCCCTGGATGAGCGAAGAACCGGGCTGCTCCGGGCTGACACCTGTGCAAC 300
OY 301 ATCAACCCCACTGCGCGCTGCGCCTAAACGCCCAAGCACTTGGGCTGGTCTGCG 360
DB 301 ATCAACCCCACTGCGCGCTGCGCCTAAACGCCCAAGCACTTGGGCTGGTCTGCG 360
OY 361 CTGCTGGGCTGTGATGCCGAGAGCAGCGCGCTTCTGCGCGGCTGGGCGGCGCT 420
DB 361 CTGCTGGGCTGTGATGCCGAGAGCAGCGCGCTTCTGCGCGGCTGGGCGGCGCT 420
OY 421 GCACCGCGCGGCTGATGCGCCAGTCCCACTTGGACATGGGCACTGATGCCGTGT 480
DB 421 GCACCGCGCGGCTGATGCGCCAGTCCCACTTGGACATGGGCACTGATGCCGTGT 480
OY 481 GGGCAGCTCTGGATGATGCTGTGAGTGTGCTTCCGTGGCAACTTGTGGGCT 540
DB 481 GGGCAGCTCTGGATGATGCTGTGAGTGTGCTTCCGTGGCAACTTGTGGGCT 540
OY 541 GAGAACTTCCACGATCTTACCCGGATGGGAAGTCTTACACTTTAACTCTGGCCT 600
DB 541 GAGAACTTCCACGATCTTACCCGGATGGGAAGTCTTACACTTTAACTCTGGCCT 600
OY 601 GATGGGAGAGAGCTCTACCACTACTAGGGGTGATGGGCAATGGGCTGGACATCATG 660
DB 601 GATGGGAGAGAGCTCTACCACTACTAGGGGTGATGGGCAATGGGCTGGACATCATG 660
OY 661 CTGACGTGACAGAGAGAAATATCTACCTGTGTGGAGGCAATGAGAGACCCCGTTT 720
DB 661 CTGACGTGACAGAGAGAAATATCTACCTGTGTGGAGGCAATGAGAGACCCCGTTT 720
OY 721 GAGTGGGGGATCCGAGTGCATACAGCCAGAGAGGCGCCCATATGATAGCTG 780
DB 721 GAGTGGGGGATCCGAGTGCATACAGCCAGAGAGGCGCCCATATGATAGCTG 780
OY 781 GGCCTTGGGGGTGTCGCCGGGTACAGAGACTTTGTTCTTGGCAGACAGAGCTGAGC 840
DB 781 GGCCTTGGGGGTGTCGCCGGGTACAGAGACTTTGTTCTTGGCAGACAGAGCTGAGC 840

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OY 841 TTCTGCGCACCGCCCTGGGGCGATTGCAAGTTGAGCATCTGAAACCCCACTATGAGCCA 900
DB 841 TTCTGCGCACCGCCCTGGGGCGATTGCAAGTTGAGCATCTGAAACCCCACTATGAGCCA 900
OY 901 GAGCCCTGTGATCCCTTAGGCTCCCCAGACCCCAAGCCCAAGCCCTTATACCTTATG 960
DB 901 GAGCCCTGTGATCCCTTAGGCTCCCCAGACCCCAAGCCCAAGCCCTTATACCTTATG 960
OY 961 GGGTGTGCGCTGGGCGGAAACCCGCTACAGTGTGCGGAAAGTGGGCTGGCGAATGCTG 1020
DB 961 GGGTGTGCGCTGGGCGGAAACCCGCTACAGTGTGCGGAAAGTGGGCTGGCGAATGCTG 1020
OY 1021 TACATGCCAGGCGAGCTGCTGAGTGTGCAAGCCCAAGCACTACAGAACTGTGCCACCG 1080
DB 1021 TACATGCCAGGCGAGCTGCTGAGTGTGCAAGCCCAAGCACTACAGAACTGTGCCACCG 1080
OY 1081 GCCATGATGCCATCTTTCGCAAGGACTGTGCGCTGCCCAACCCGTGCGCAGCAG 1140
DB 1081 GCCATGATGCCATCTTTCGCAAGGACTGTGCGCTGCCCAACCCGTGCGCAGCAG 1140
OY 1141 CGCTAGCGCAAGGAGCTGCTGATGCTGGGATCCCGAGCGCGCGCGCGCTTCTG 1200
DB 1141 CGCTAGCGCAAGGAGCTGCTGATGCTGGGATCCCGAGCGCGCGCGCGCTTCTG 1200
OY 1201 GCCCGAAGCTCAACCGCAGAGGCTCTACATCCGCGAGAAAGTGGCCCTGGACATC 1260
DB 1201 GCCCGAAGCTCAACCGCAGAGGCTCTACATCCGCGAGAAAGTGGCCCTGGACATC 1260
OY 1261 TTTCTTAGAGCCCTCACTATGAGACCGTGGAGCAAGAAAGGCTATGAGATGTACAG 1320
DB 1261 TTTCTTAGAGCCCTCACTATGAGACCGTGGAGCAAGAAAGGCTATGAGATGTACAG 1320
OY 1321 CTGCTTGGTGAATGAGGGGCGAGATGGGCGCTTTCATCGGGGCGAGCTGCTCAACATC 1380
DB 1321 CTGCTTGGTGAATGAGGGGCGAGATGGGCGCTTTCATCGGGGCGAGCTGCTCAACATC 1380
OY 1381 CTGAGATCTAGACTTCTGTGAGGTGTTCGAGCAAGATCTGGGATATTTCTG 1440
DB 1381 CTGAGATCTAGACTTCTGTGAGGTGTTCGAGCAAGATCTGGGATATTTCTG 1440
OY 1441 AACGCAAGCACTCCCAAGGCACTCCAGCAACCAATCTGCTTCAAGAAAGGCTGGGCA 1500
DB 1441 AACGCAAGCACTCCCAAGGCACTCCAGCAACCAATCTGCTTCAAGAAAGGCTGGGCA 1500
OY 1501 CATGGAACCAAGTTCCCACTCAGCTTGGGCGCCAGACCTCCACACCTTCTCTG 1560
DB 1501 CATGGAACCAAGTTCCCACTCAGCTTGGGCGCCAGACCTCCACACCTTCTCTG 1560
OY 1561 GTCAACCAAGACTCTCTCGCCTCCACCGCACTGTACTTGTACACAGCTCTAGACC 1620
DB 1561 GTCAACCAAGACTCTCTCGCCTCCACCGCACTGTACTTGTACACAGCTCTAGACC 1620
OY 1621 TGTCTGTGTGTCTCTCGGAGCGCCGCTGTACATCTGGGAATGCTTGAAGCTTGA 1680
DB 1621 TGTCTGTGTGTCTCTCGGAGCGCCGCTGTACATCTGGGAATGCTTGAAGCTTGA 1680
OY 1681 CTTTTCCTTTCACCCCAATTAAGTCTTAATGATCAAAAAAAAAAAAAA 1732
DB 1681 CTTTTCCTTTCACCCCAATTAAGTCTTAATGATCAAAAAAAAAAAAAA 1732

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RESULT 2  
AA517126  
ID AA517126 standard; cDNA; 1732 BP.  
XX  
XX AA517126;  
XX  
XX 14-FEB-2002 (first entry)  
XX  
XX Human cDNA encoding acid sensing ion channel subunit 3, ASIC3A.  
XX  
XX Human; ss; acid sensing ion channel; ASIC3A; analgesic; anti-HIV;  
KW

neuroprotective; nootropic; antiparkinsonian; anticonvulsant;  
cerebroprotective; cardiant; antianal; hypotensive;  
antithrombotic; vasotropic; tranquilizer; antidepressant;  
chronic pain; neuropathic pain; diabetes; cancer; AIDS;  
acquired immunodeficiency syndrome; neurodegenerative disease;  
Alzheimer's disease; Parkinson's disease; Huntington's disease;  
Creutzfeldt-Jacob disease; amyotrophic lateral sclerosis; dementia;  
convulsion; epilepsy; stroke; anxiety; depression; angina;  
cardiovascular disease; congestive heart failure; vasoconstriction;  
hypertension; atherosclerosis; restenosis; bleeding; gene therapy.

Homo sapiens.

Key Location/Qualifiers  
CDS 22..1617  
FT /tag-a  
FT /product= "ASIC3A"

WO200181570-A2.  
01-NOV-2001.  
20-APR-2001; 2001WO-CA00561.  
20-APR-2000; 2000CA-2304494.  
(UWMC-) UNIV MCGILL.  
Seguela P, Babiniski K;  
WPI: 2002-055353/07.  
P-PSDB: AAU10904.

New heteromultimeric proton-gated ion channel for diagnosing, treating  
diseases associated with expression of the channel e.g.  
neurodegenerative diseases, comprises two different types of acid  
sensing ion channel subunits

Claim 7; Page 96-97; 105pp; English.

The invention relates to a protein complex forming a heteromultimeric  
amiloride- and gadolinium-sensitive proton-gated cation channel  
(ASIC-2S.2), where the individual components of the heteromultimeric  
channel include the acid sensing ion channel (ASIC2A and ASIC3 protein  
or their variants having 80% sequence identity, the channel being  
activated by protons, acids, low pH solutions, the nucleic acids  
encoding the subunits, a recombinant bicistronic vector comprising a  
nucleic acid encoding at least two individual subunits or variants of  
ASIC-2S.2, a host cell comprising the vector, an antibody raised against  
one of the subunits or a domain which is capable of disrupting assembly  
of the ion channel and ant/agonists of the ion channel. The polypeptides  
and polynucleotides are useful for diagnosing a disease or a  
susceptibility to a disease in a subject related to expression or  
activity of the heteromultimeric channel (e.g. by gene therapy using the  
vector). Such diseases include chronic pain, neuropathic pain such as  
diabetic, cancer- and AIDS (acquired immunodeficiency syndrome)-related,  
neurodegenerative diseases such as Alzheimer's disease, Parkinson's  
disease, Huntington's disease, Creutzfeldt-Jacob disease, and amyotrophic  
lateral sclerosis and dementias, including AIDS-related as well as  
convulsions, epilepsy, stroke, anxiety and depression. They are also  
useful for treating cardiovascular diseases such as angina, congestive  
heart failure, vasoconstriction, hypertension, atherosclerosis,  
restenosis and bleeding. ASIC-2S.2 plays a role in the regulation of  
neurotransmitter release, neuronal excitability or excitotoxicity and is  
useful in screening for compounds that regulate neurotransmitter release,  
CC synaptic efficacy, neuroexcitability or neurotoxicity. The present  
sequence encodes human ASIC3A.

Sequence 1732 BP; 326 A; 601 C; 484 G; 321 T; 0 other;

Query Match 100.0%; Score 1732; DB 24; Length 1732;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCGCAGCAGCGGCTTCTGCGCATGAAAGCCACCTCAGGCCAGAGAGGCGCGGGCAG 60  
1 TCGCAGCAGCGGCTTCTGCGCATGAAAGCCACCTCAGGCCAGAGAGGCGCGGGCAG 60  
1 TCGCAGCAGCGGCTTCTGCGCATGAAAGCCACCTCAGGCCAGAGAGGCGCGGGCAG 60  
61 CCTCGGACATCGCGCTGTTCGACAGCACTGCTGATCAGAGGCGTGGGACAGCTTC 120  
61 CCTCGGACATCGCGCTGTTCGACAGCACTGCTGATCAGAGGCGTGGGACAGCTTC 120  
121 GGGCCAGCAGCCTGAGCCTGCGCGCGGGGAGTGTGGGACAGCGCGCTGCTGTACGTG 180  
121 GGGCCAGCAGCCTGAGCCTGCGCGCGGGGAGTGTGGGACAGCGCGCTGCTGTACGTG 180  
181 GGCACCTTCTTACACAGGTGGGTGAGAGGTGGCTTACTACAGGAGTTCACACCCAG 240  
181 GGCACCTTCTTACACAGGTGGGTGAGAGGTGGCTTACTACAGGAGTTCACACCCAG 240  
241 ACTGCCCTGGATGAGGAGAGAAAGCCACCGGCTGCTTCCCGGCTGTACACCTGTGCAAC 300  
241 ACTGCCCTGGATGAGGAGAGAAAGCCACCGGCTGCTTCCCGGCTGTACACCTGTGCAAC 300  
301 ATCAACCCACTGCGCGCTGCGGCTTAACGCCCAAGACCTGCACTGGGCTGGCTGCG 360  
301 ATCAACCCACTGCGCGCTGCGGCTTAACGCCCAAGACCTGCACTGGGCTGGCTGCG 360  
361 CTGCTGGGCTGGATCCCGCAGAGCAGCGCGCTTCTGCGGCGCGTGGGCGCGCCCT 420  
361 CTGCTGGGCTGGATCCCGCAGAGCAGCGCGCTTCTGCGGCGCGTGGGCGCGCCCT 420  
421 GCACCGCGCGGCTTCAATGCGCAAGTCCACCTTTCGATGAGTGGCAATCTATGCGCGCT 480  
421 GCACCGCGCGGCTTCAATGCGCAAGTCCACCTTTCGATGAGTGGCAATCTATGCGCGCT 480  
481 GGGCAGCTCCCTGGATGATGATGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
481 GGGCAGCTCCCTGGATGATGATGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
541 GAGAACTTCAACCAAGATCTTCAACCGGATGGGAAATGCTATCACTTAACTTGGCGCT 600  
541 GAGAACTTCAACCAAGATCTTCAACCGGATGGGAAATGCTATCACTTAACTTGGCGCT 600  
601 GATGGGGCAGAGTGTCTCAACCTACTAGGAGGATGGATGGATGGATGGATGGATGGAT 660  
601 GATGGGGCAGAGTGTCTCAACCTACTAGGAGGATGGATGGATGGATGGATGGATGGAT 660  
661 CTGACGTGCGAGCAGAGGAAATATCTACTGTTGTGGAGGAGACAAATGAGAGACCCGTTT 720  
661 CTGACGTGCGAGCAGAGGAAATATCTACTGTTGTGGAGGAGACAAATGAGAGACCCGTTT 720  
721 GAGGTGGGATCCGATGCAATCCACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
721 GAGGTGGGATCCGATGCAATCCACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
781 GGGTGGGAGTGTCCCGGGGCTACAGACCTTGTGTTTGGCAGAGAGAGAGAGAGAGAG 840  
781 GGGTGGGAGTGTCCCGGGGCTACAGACCTTGTGTTTGGCAGAGAGAGAGAGAGAGAG 840  
841 TTCTCTCCACCGCGCTGGGGGATTCAGATCTCTGAACTCTGAAACCCCAACTATGAGCCA 900  
841 TTCTCTCCACCGCGCTGGGGGATTCAGATCTCTGAACTCTGAAACCCCAACTATGAGCCA 900  
901 GAGCCTCTGATATCCCTAGGCTTCCCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 960  
901 GAGCCTCTGATATCCCTAGGCTTCCCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 960  
961 GAGCCTCTGATATCCCTAGGCTTCCCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1020  
961 GAGCCTCTGATATCCCTAGGCTTCCCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1020  
1021 TACATGCCAGGCGAGCTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 1080  
1021 TACATGCCAGGCGAGCTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 1080

QY	1081	GCATAGATGTCATCTCTTCCGAAAGGATCGTGGGCGCTGGCCCAACCCGTCGGCCAGCAGC	1140
Db	1081	GCCATAGATGTCATCTCTTCCGAAAGGATCGTGGGCGCTGGCCCAACCCGTCGGCCAGCAGC	1140
QY	1141	GCGTACGCCAAGGAGCTCTCCATGCTGGGATCCGACGGCGCGCCGCGGCTTCCCTG	1200
Db	1141	GCGTACGCCAAGGAGCTCTCCATGCTGGGATCCGACGGCGCGCGCGGCTTCCCTG	1200
QY	1201	GCCCGGAAGCTCAACCCGACGAGAGGCTACATGCGCGAAGACGTGTGGCTTGGACATC	1260
Db	1201	GCCCGGAAGCTCAACCCGACGAGAGGCTACATGCGCGAAGACGTGTGGCTTGGACATC	1260
QY	1261	TTCTTTGAGGCGCCCTCAACTATGAGACCGTGGAGCAAGAAAGAGCCATAGATGTCAAG	1320
Db	1261	TTCTTTGAGGCGCCCTCAACTATGAGACCGTGGAGCAAGAAAGAGCCATAGATGTCAAG	1320
QY	1321	CTGCTTGCTGACATTTGGGGGCGAGATGGGCTTTTCATCGGGGCCAGCCTGCTACATC	1380
Db	1321	CTGCTTGCTGACATTTGGGGGCGAGATGGGCTTTTCATCGGGGCCAGCCTGCTACATC	1380
QY	1381	CTCGAGATCCAGAGACTCTCTGTGAGGATTTCCGAGACAAAGTCTCTGGGATATTCTGG	1440
Db	1381	CTCGAGATCCAGAGACTCTCTGTGAGGATTTCCGAGACAAAGTCTCTGGGATATTCTGG	1440
QY	1441	AACGACAGCACTCTCCAAAGGCACTCCAGCACCACCAATCTCTTCAGAAAGGCTGGGAGC	1500
Db	1441	AACGACAGCACTCTCCAAAGGCACTCCAGCACCACCAATCTCTTCAGAAAGGCTGGGAGC	1500
QY	1501	CATGAAACCAAGTTCCGCCACCTGAGGCTGGGGCCGACAGCCTCCACCCCTCCGTGACC	1560
Db	1501	CATGAAACCAAGTTCCGCCACCTGAGGCTGGGGCCGACAGCCTCCACCCCTCCGTGACC	1560
QY	1561	GTCACCAAGACTCTCTCCGCTCCCAACGCACTGCTACTTGTGCACAGCTTAGACC	1620
Db	1561	GTCACCAAGACTCTCTCCGCTCCCAACGCACTGCTACTTGTGCACAGCTTAGACC	1620
QY	1621	TGCTGTCTGTCTCTCGGAGCCCCCGCCCTGACATCTCTGACATGCTGACCTGACAGTAG	1680
Db	1621	TGCTGTCTGTCTCTCGGAGCCCCCGCCCTGACATCTCTGACATGCTGACCTGACAGTAG	1680
QY	1681	CTTTTCGCTTTCACCCCAATAAAGTCTAATGATCATCAAAAAAAAAAAAAA	1732
Db	1681	CTTTTCGCTTTCACCCCAATAAAGTCTAATGATCATCAAAAAAAAAAAAAA	1732
RESULT 3			
AAZ61203			
ID	AAZ61203 standard; cDNA; 1736 BP.		
XX	AAZ61203;		
AC			
XX	30-MAY-2000 (first entry)		
DT			
XX	cDNA encoding a human acid-sensitive cationic channel 3 (hASIC3).		
DE			
XX			
XX	Neuronal acid-sensitive cation channel; ASIC; ASIC 3;		
KW	proton-gated cation channel; biophysical desensitization; amiloride;		
KW	cation transport channel; acid sensor; pH detection; ds.		
XX			
XX	Homo sapiens.		
OS			
XX			
PN	WO200008149-A2.		
XX			
PD	17-FEB-2000.		
XX			
PF	05-AUG-1999; 99MO-IB01445.		
XX			
PR	05-AUG-1998; 98US-0095408.		
XX			

[illegible]

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Db 601 GGGCAGAGCTGCTCACCACTACTAGGGGTGGCATGGCAATGGGCTGGACATCATGCTGG 660
Oy 665 ACGTCACACGAGAGAGAAATATCTACTGTGTGTGAGAGACAAATAGAGAGACCCGTTTGAGG 724
Db 661 ACGTGCACACGAGAGAGAAATATCTACTGTGTGTGAGAGACAAATAGAGAGACCCGTTTGAGG 720
Oy 725 TGGGGATCCGAGTGCAGATCCACAGCCAGAGAGAGCCGCCCTCATGCTAGCTGGGGCT 784
Db 721 TGGGATCCGAGTGCAGATCCACAGCCAGAGAGAGCCGCCCTCATGCTAGCTGGGGCT 780
Oy 785 TGGGGGTGTCCCGGGGCTACAGACCTTTGTTTCTTGCCAGCAGCAGCAGCTGACTTCC 844
Db 781 TGGGGGTGTCCCGGGGCTACAGACCTTTGTTTCTTGCCAGCAGCAGCAGCTGACTTCC 840
Oy 845 TGCCACCCGCTGGGGGCTGTCAGTTCAGCATCTCTGAAACCCCACTATGAGCCAGAC 904
Db 841 TGCCACCCGCTGGGGGCTGTCAGTTCAGCATCTCTGAAACCCCACTATGAGCCAGAC 900
Oy 905 CCTGTGATCCCTTAGGCTCCCGCCAGCCCGCCAGCCCTCCATACCTTATGGGGT 964
Db 901 CCTGTGATCCCTTAGGCTCCCGCCAGCCCGCCAGCCCTCCATACCTTATGGGGT 960
Oy 965 GTCCGCTGGGCTGCGAAACCCGCTACGTGCTCGGAAAGTGGGCTGCCGATGTGTACA 1024
Db 961 GTCCGCTGGGCTGCGAAACCCGCTACGTGCTCGGAAAGTGGGCTGCCGATGTGTACA 1020
Oy 1025 TGCCAGGCGACGTGCAGATGTGCAGCCGCCAGCAGTACAGAACTGTGCCACCCGGCCA 1084
Db 1021 TGCCAGGCGACGTGCAGATGTGCAGCCGCCAGCAGTACAGAACTGTGCCACCCGGCCA 1080
Oy 1085 TAGATGCATCTTGTGGCAAGGACTGTGTGGCTGGCCCAACCCGTGGCGACAGCGCT 1144
Db 1081 TAGATGCATCTTGTGGCAAGGACTGTGTGGCTGGCCCAACCCGTGGCGACAGCGCT 1140
Oy 1145 ACGCCAAAGAGCTCTCAATGTGTGCGGATCCGAGCCGCGCCGCGGCTCTTGAGGCC 1204
Db 1141 ACGCCAAAGAGCTCTCAATGTGTGCGGATCCGAGCCGCGCCGCGGCTCTTGAGGCC 1200
Oy 1205 GGAAGCTCAACCGCAGCGAGGCTCTACATGCGGAGAGACGTGTGGCCCTTGACATCTTCT 1264
Db 1201 GGAAGCTCAACCGCAGCGAGGCTCTACATGCGGAGAGACGTGTGGCCCTTGACATCTTCT 1260
Oy 1265 TTGAGGCTCTCAATGTAGAACCGTGGAGCAGAAAGAGCCCTATAGATGTAGAGCTGC 1324
Db 1261 TTGAGGCTCTCAATGTAGAACCGTGGAGCAGAAAGAGCCCTATAGATGTAGAGCTGC 1320
Oy 1325 TTGTGACATTTGGGGGCGAGATGGGCTTTTCATGSGGGCGAGCTGCTCACATCTCTG 1384
Db 1321 TTGTGACATTTGGGGGCGAGATGGGCTTTTCATGSGGGCGAGCTGCTCACATCTCTG 1380
Oy 1385 AGATCTTAGACTACTCTGTGTGAGTGTTCGAGACAAAGTCTCTGGGATATTTCTGGAACC 1444
Db 1381 AGATCTTAGACTACTCTGTGTGAGTGTTCGAGACAAAGTCTCTGGGATATTTCTGGAACC 1440
Oy 1445 GACACACTTCCCAAGGCACTTCACACCAATCTGCTTCAGAAAGGCTGGGCAAGCCATC 1504
Db 1441 GACACACTTCCCAAGGCACTTCACACCAATCTGCTTCAGAAAGGCTGGGCAAGCCATC 1500
Oy 1505 GAACCAAGTTCCCACTCAGCCTGAGGCGCCAGACCTCCACCCCTCCCTTGCCGCTA 1564
Db 1501 GAACCAAGTTCCCACTCAGCCTGAGGCGCCAGACCTCCACCCCTCCCTTGCCGCTA 1560
Oy 1565 CCAAGACTCTCTCGGCTCCACCGCAGCTGTCTTGTCTACACAGCTCTAGACCTGCT 1624
Db 1561 CCAAGACTCTCTCGGCTCCACCGCAGCTGTCTTGTCTACACAGCTCTAGACCTGCT 1620
Oy 1625 GTCTGTGCTCTGAGAGCCCGCCGCTGACATCTGTGACAAAGCTCTAGCCTGACGTAGCTT 1684
Db 1621 GTCTGTGCTCTGAGAGCCCGCCGCTGACATCTGTGACAAAGCTCTAGCCTGACGTAGCTT 1680
Oy 1685 TCCGCTTTCACCCCAATTAAGTCTTAATGATCAAAAAA 1732

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Db 1681 TCCGCTTTCACCCCAATTAAGTCTTAATGATCAAAAAA 1728

RESULT 4
AAV84191
ID AAV84191 standard; cDNA to mRNA; 1650 BP.
XX
AC AAV84191;
XX
DT 29-MAR-1999 (first entry)
DE
DE Sodium channel receptor hSINAC1 splice variant.
KM hSINAC1; sodium channel receptor; human; algisia; analgesia;
KM ds; cyclic; circular.
XX
OS Homo sapiens.
PN W09854316-A1.
PD 03-DEC-1998.
XX
PF 15-MAY-1998; 98WO-EP02884.
PR 30-MAY-1997; 97EP-0401196.
XX
PA (SYNO ) SYNTHELABO.
PI
PI Bernard F, Graham D, Renard S;
XX
DR WPI: 1999-070215/06.
DR P-PSDB: AAM88252.
XX
PT A new sodium channel receptor - useful for, e.g. treatment of
PT neuronal degenerate problems, Alzheimer's, Parkinson's disease and
PT morphine dependence
XX
PS Claim 26; Page 43-46; 63pp; English.
XX
CC This is the coding region of a polynucleotide encoding a splice
CC variant (see AAM88252) of a new human sodium channel receptor (see
CC AAM88250), termed hSINAC1. The polynucleotide was obtained from
CC dorsal root ganglia cDNA by PCR amplification using primers (see
CC V84120-21) based on the hSINAC1 polynucleotide (see AAV84189).
CC hSINAC1 is a member of a new class of sodium channel proteins that
CC may be responsible for some nervous system transmissions, or may be
CC used as a target to regulate some transmissions linked to various
CC pathologies. The splice variant cDNA has a 79-nucleotide insert in
CC the 3' portion of the coding region. This alters the reading
CC frame. As dorsal root ganglia are involved in pain perception, the
CC splice variant protein is expected to have a function linked to
CC algisia or analgesia.
XX
SQ Sequence 1650 BP; 298 A; 575 C; 473 G; 304 T; 0 other;

Query Match 91.7%; Score 1588.8; DB 20; Length 1650;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1623; Conservative 0; Mismatches 7; Indels 20; Gaps 1;

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Dp	181	GCTGAGAGGtGtGcCTACTACAGGAGtTCCACACAGAcTCCcCTGGATGAGGAGAA	24
Qy	262	AGCCACGcGCTGCTTCtCCGgGCTGTACcCTTGCAATCAACCACTGGCGGCTCG	321
Dp	241	AGCCACGcGCTCATCTTCcCGGcGTGTACcCTTGCAATCAACCACTGGCGGCTTCG	300
Qy	342	GCcCTTAAGcGcCAAGAcCTGTGCATGTGGGtCGGGGtCTGGcCTGGTGGCCGATCCCGCA	381
Dp	301	GCcCTTAAGcGcCAAGAcCTGTGCATGTGGGtCGGGGtCTGGcCTGGTGGcCTCGGATCCCGCA	360
Qy	382	GAGCAcGcGcCTTCtTGcGCGcCTTGcGGcGcGcGcGcGcCTTGcACGcGcGCTTCATGcCC	441
Dp	361	GAGCAcGcGcGcCTTCtTGcGCGcGcCTTGcGGcGcGcGcGcGcCTTGcACGcGcGCTTCATGcCC	420
Qy	442	AGTCCACCTTTGACATGTGGGCAACTTATGCCGTGTGGGCACTTCCTGGATGCATG	501
Dp	421	AGTCCACCTTTGACATGTGGGCAACTTATGCCGTGTGGGCACTTCCTGGATGCATG	480
Qy	502	CTGcTGAGAcCTGCCTTCcCGGgGCAACCTTGtGGGcCTGAGAACTTCACAGAcCTTC	561
Dp	481	CTGcTGAGAcCTGCCTTCcCGGgGCAACCTTGtGGGcCTGAGAACTTCACAGAcCTTC	540
Qy	562	ACCCGgATGGAAAGTcCTACACTTTTAACTGTGGcGTGTAGGGGAGAGcGTGTCAAC	621
Dp	541	ACCCGgATGGAAAGTcCTACACTTTTAACTGTGGcGTGTAGGGGAGAGcGTGTCAAC	600
Qy	622	ACTACTAGGGTGGCATGTGGGCAATGTGGCTGGACATCATGTGGACGTGCACAGAGAA	681
Dp	601	ACTACTAGGGTGGCATGTGGGCAATGTGGCTGGACATCATGTGGACGTGCACAGAGAA	660
Qy	682	TATCTACTGTGTGGAGGAGCAATGAGAGAACCCCGTTTGTAGGTGGGAGATCCGAGTGCAG	741
Dp	661	TATCTACTGTGTGGAGGAGCAATGAGAGAACCCCGTTTGTAGGTGGGAGATCCGAGTGCAG	720
Qy	742	ATCCACAGCCAGAGAGAGcCGCCCATCATGATCAGCTGGGCTTGGGGTGTCCCGGGcC	801
Dp	721	ATCCACAGCCAGAGAGAGcCGCCCATCATGATCAGCTGGGCTTGGGGTGTCCCGGGcC	780
Qy	802	TACCAgACCTTTGTtTTCTTGcCAgACAGcAGcTGAcCTTCcTGcCACCGcCTGTGGGcC	861
Dp	781	TACCAgACCTTTGTtTTCTTGcCAgACAGcAGcAGcTGAcCTTCcTGcCACCGcCTGTGGGcC	840
Qy	862	GATTGcAGTTTAgATCTCTGAAACCCCACTATGAGCCAGAGCCCTGTATCCCTAGGC	921
Dp	841	GATTGcAGTTTAgATCTCTGAAACCCCACTATGAGCCAGAGCCCTGTATCCCTAGGC	900
Qy	922	TCCCCAGcCCcCAGcCCcCAGcCCcCTCCCTATACcCTTATGGGtGTGTGcCTTGcCTTGcGNA	981
Dp	901	TCCCCAGcCCcCAGcCCcCAGcCCcCTCCCTATACcCTTATGGGtGTGTGcCTTGcCTTGcGNA	960
Qy	982	ACCCGcCTACGTGTcGGAAGTGGcGTGGcGCGAATGTGTACATGcCAGcGcAGcGTGCCA	1041
Dp	961	ACCCGcCTACGTGTcGGAAGTGGcGTGGcGCGAATGTGTACATGcCAGcGcAGcGTGCCA	1020
Qy	1042	GtGTGcAGcCCcCAGcAGTACAAGAACTGTGTGCCACCcCGGCATAGATCCATCTCTGGC	1101
Dp	1021	GtGTGcAGcCCcCAGcAGTACAAGAACTGTGTGCCACCcCGGCATAGATCCATCTCTGGC	1080
Qy	1102	AAGAGAcTGTGcGcCTGCcCCCAACCGGTGGcGcCAGAGcGcGTACGcCAAGAGAcCTTC	1161
Dp	1081	AAGAGAcTGTGcGcCTGCcCCCAACCGGTGGcGcCAGAGcGcGTACGcCAAGAGAcCTTC	1140
Qy	1162	ATGTGTGGGATCCCGAGcCGcGCGcGCGcGCGcCTTCGTGGcCGGAAAGCTCAACCGcAGc	1221
Dp	1141	ATGTGTGGGATCCCGAGcCGcGCGcGCGcGCGcCTTCGTGGcCGGAAAGCTCAACCGcAGc	1200
Qy	1222	GAGcCTTACATCGCGGAGAACTGTGTGGcCTTGAGAcATCTTCTTTGAGGcCCTCACTAT	1281
Dp	1201	GAGcCTTACATCGCGGAGAACTGTGTGGcCTTGAGAcATCTTCTTTGAGGcCCTCACTAT	1260
Qy	1282	GAGAGcGTGGGAGAGAAAGGcCTTATGAGATGTACAGAcCTTGtGTGACATTGTGGGGcC	1341
Dp	1261	GAGAGcGTGGGAGAGAAAGGcCTTATGAGATGTACAGAcCTTGtGTGACATTGTGGGGcC	1320

QY	1342	CAGATGGGCGCTTTTCATCGGGGGCAGCGTCCTACCATCTCGAGATCTCTAATCAATCCG	1401
Db	1331	CAGATGGGGCGCTTTCATCGGGGGCAGCGCTCTCATCATCTCTGAGATCTCTAATCAATCCG	1386
QY	1402	TGTAGGTGTGTTCCGAGACAAGTCTCTGGGATATTGTTGGAAACCGACGACATCCCAAGG	1461
Db	1381	TGTAGGTGTTCGAGACAAGGTCTCTGGGATATTGTTGGAAACCGACGACATCCCAAGG	1440
QY	1462	CACATCGACGACCAATCTGTTTCAGGAAGGCTGGGACGCGATCGAACCAGATTCCCGAC	1521
Db	1441	CACATCGACGACCAATCTGTTTCAGGAAGGCTGGGACGCGATCGAACCAGATTCCCGAC	1500
QY	1522	CTCAGCGCTGGGCC-----AGACCTCCACCCCTCCCTTGGCG	1561
Db	1501	CTCAGCGCTGGGCCCCACACACTCTGCTCTGTTCCGAAGACCTCCACCCCTCCCTTGGCG	1560
QY	1562	TCACACAGACGCTCTCGGCTCTCCACACGGACCGTAACCTGTCAACACAGCTCTAGACCT	1621
Db	1561	TCACACAGACGCTCTCGGCTCTCCACACGGACCGTAACCTGTCAACACAGCTCTAGACCT	1620
QY	1622	GCTCTCTGTGTCCTCGAGGCCCGCCCTGA	1651
Db	1621	GCTCTCTGTGTCCTCGAGGCCCGCCCTGA	1650

XX	AAV84189	
XX	AAV84189 standard; cDNA to mRNA; 1723 BP.	
XX	AAV84189;	
XX	29-MAR-1999 (first entry)	
XX	Sodium channel receptor hSLNAC1 cDNA.	
XX	hSLNAC1; sodium channel receptor; human; neurodegeneration;	
XX	Alzheimer's disease; Parkinson's disease; morphine dependence;	
XX	chorea; muscular spasm; epilepsy; stroke; cardiac disease;	
XX	schizophrenia; depression; nicotine dependence;	
XX	amortrophic lateral sclerosis; multiple sclerosis; inflammation;	
XX	pain; cancer; obesity; neurotransmitter; analgesic; anaesthesia;	
XX	ds; cyclic; circular.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	13..1644
XX		/**tag= a
XX	W09854316-A1.	
XX	03-DEC-1998.	
XX	15-MAY-1998; 98WO-EP02884.	
XX	30-MAY-1997; 97EP-0401196.	
XX	(SYNO ) SYNTHETLABO.	
XX	Besnard F, Graham D, Renard S;	
XX	WPI: 1999-070215/06.	
XX	P-PsDB: AAW88250.	
XX	A new sodium channel receptor - useful for, e.g. treatment of	
XX	neuronal degenerate problems, Alzheimer's, Parkinson's disease and	
XX	morphine dependence	
XX	Claim 3; Page 31-34; 63pp; English.	
XX	This CDNA clone, designated p3SLNAC1, codes for a new human sodium	
XX	channel receptor (see AAW88250) termed hSLNAC1. This is a member of	

CC a new class of sodium channel proteins that may be responsible for  
CC some nervous system transmissions, or may be used as a target to  
CC regulate some transmissions linked to various pathologies.  
CC p3SLIMAC1 (ATCC 97987) was isolated from a human cerebellum cDNA  
CC library following an expressed sequence tag database screening.  
CC Methods for producing hSLIMAC1 polypeptides by recombinant methods  
CC are disclosed. Host cells expressing hSLIMAC1 can be used to screen  
CC for agonists or antagonists of hSLIMAC1. Such compounds can be used  
CC to treat neurodegeneration, hyperalgesia, Alzheimer's disease,  
CC Parkinson's disease, chorea, muscular spasm, epilepsy, stroke,  
CC cardiac diseases, schizophrenia, depression, nicotine dependence,  
CC morphine dependence, amyotrophic lateral sclerosis, multiple  
CC sclerosis, inflammation, pain, cancer and obesity, to mimic or  
CC antagonise the effects of endogenous transmitter peptides,  
CC opioids or anti-opioids, to alter gustative perception, to cause  
CC analgesia or anaesthesia, or to diagnose or treat any disorder  
CC related to abnormal expression of hSLIMAC1.

XX Sequence 1723 BP; 331 A; 586 C; 483 G; 323 T; 0 other;

Query Match 91.4%; Score 1583.8; DB 20; Length 1723;

Best Local Similarity 96.2%; Pred. No. 0;

Matches 1657; Conservative 0; Mismatches 7; Indels 59; Gaps 1;

QY 10 GGGGTTCTGGCCATGAGAGCCACCTAGGCCAGAGAGCCCGGGGCGACCCCTGGGAC 69  
DB 1 GGGGTTCTGGCCATGAGAGCCACCTAGGCCAGAGAGCCCGGGGCGACCCCTGGGAC 60  
QY 70 ATCCGCGTTTGGCCAGCACTGCTGATGACAGGGGCTGGGCGACCTTTGGGCGGAGC 129  
DB 61 ATCCGCGTTTGGCCAGCACTGCTGATGACAGGGGCTGGGCGACCTTTGGGCGGAGC 120  
QY 130 AGCTGAGCCTGCGCGGGGATGTCGCGAGCGGCGCTGCTGCTGATGAGTGGCCTTTC 189  
DB 121 AGCTGAGCCTGCGCGGGGATGTCGCGAGCGGCGCTGCTGCTGATGAGTGGCCTTTC 180  
QY 190 CTCTACAGAGTGGTGAAGGGGTGCTACTACAGGAGTTCACACAGACTGGCCCTG 249  
DB 181 CTCTACAGAGTGGTGAAGGGGTGCTACTACAGGAGTTCACACAGACTGGCCCTG 240  
QY 250 GATGAGCGAGAAAGCCAGCGGCTGCTTCCCGGCTGTCACCCCTGTGCAACATCAACCA 309  
DB 241 GATGAGCGAGAAAGCCAGCGGCTGCTTCCCGGCTGTCACCCCTGTGCAACATCAACCA 300  
QY 310 CTGCGCGGCTCGGCGCTTAACGCCCAAGACCTGACCTGGGCTGGCTGCTGGGCTGG 369  
DB 301 CTGCGCGGCTCGGCGCTTAACGCCCAAGACCTGACCTGGGCTGGCTGCTGGGCTGG 360  
QY 370 CTGAGATCCCGCAGAGACCGCGCTTCTGCGGCGCCCTGGGCGGCGCCCTGACCGGCC 429  
DB 361 CTGAGATCCCGCAGAGACCGCGCTTCTGCGGCGCCCTGGGCGGCGCCCTGACCGGCC 420  
QY 430 GGGCTTCATGCCAGTCCACCTTTGACATGGCGCAACTGTATGCCGTGGGCACTCC 489  
DB 421 GGGCTTCATGCCAGTCCACCTTTGACATGGCGCAACTGTATGCCGTGGGCACTCC 480  
QY 490 CTGAGATGAATGCTGCTGAGACTGCTGCTGCGGCCAAGCTTGTGGGCTGGAATTC 549  
DB 481 CTGAGATGAATGCTGCTGAGACTGCTGCTGCGGCCAAGCTTGTGGGCTGGAATTC 540  
QY 550 ACCAGATCTTCCACCGGATGGGAAGTGTACACATTTAACTCTGGCGTGAATGGGCA 609  
DB 541 ACCAGATCTTCCACCGGATGGGAAGTGTACACATTTAACTCTGGCGTGAATGGGCA 600  
QY 610 GAGCTGCTACCACTAGGGGTGGCATGGGCAATGGGCTGGACATCATGCTGAGAGCTG 669  
DB 601 GAGCTGCTACCACTAGGGGTGGCATGGGCAATGGGCTGGACATCATGCTGAGAGCTG 660  
QY 670 CAGCAGAGGAATATCTACTGCTGAGAGGAGAAATGAGAGAGACCCCGTTTGAAGTGGG 729  
DB 661 CAGCAGAGGAATATCTACTGCTGAGAGGAGAAATGAGAGAGACCCCGTTTGAAGTGGG 720  
QY 730 ATCCGAGTGCAGATCCACAGCCAGAGAGGCCCATCATCATGAGTGGGCTTGGG 789

DB 721 ATCCGAGTGCAGATCCACAGCCAGAGAGACCCCATCATCATGAGTGGGCTTGGG 780  
QY 790 GTGTCCCGGGGCTACCAAGACTTTGTTCTTGGCAGCAGCAGCAGTGAAGTCTTGCCA 849  
DB 781 GTGTCCCGGGGCTACCAAGACTTTGTTCTTGGCAGCAGCAGCAGTGAAGTCTTGCCA 840  
QY 850 CCGCCCTGGGCGATTGCAATGATCTCTTAACCCCACTATAGCAGACGCCCTCT 909  
DB 841 CCGCCCTGGGCGATTGCAATGATCTCTTAACCCCACTATAGCAGACGCCCTCT 900  
QY 910 GATCCCTTGGGCTCCCGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 969  
DB 901 GATCCCTTGGGCTCCCGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 960  
QY 970 CTGGCCTGGGAAACCCGCTACGTGAGTGGGAGTGGGAGTGGGAGTGGTATGATGCCA 1029  
DB 961 CTGGCCTGGGAAACCCGCTACGTGAGTGGGAGTGGGAGTGGGAGTGGTATGATGCCA 1020  
QY 1030 GCGCAGTGGCAGTGTGACAGCCCGCAGCAGTACAGAACTGTCCCAACCGGCTATGAT 1089  
DB 1021 GCGCAGTGGCAGTGTGACAGCCCGCAGCAGTACAGAACTGTGTCCCAACCGGCTATGAT 1080  
QY 1090 GCCATCTTGGGCAAGGACTGTGGGCTGGCCCAACCCGCGGCGCAAGCGGCTTACGCC 1149  
DB 1081 GCCATCTTGGGCAAGGACTGTGGGCTGGCCCAACCCGCGGCGCAAGCGGCTTACGCC 1140  
QY 1150 AAGGAGCTCTCCATGTTGCGGATCCCGAGCGCGCGCGCGGCTTCTGGCGCGGAAG 1209  
DB 1141 AAGGAGCTCTCCATGTTGCGGATCCCGAGCGCGCGCGCGGCTTCTGGCGCGGAAG 1200  
QY 1210 CTCAACCGCAGCGAGGCTTACATCGCGGAGAACGTGTGGCTGGACATCTTCTTGAAG 1269  
DB 1201 CTCAACCGCAGCGAGGCTTACATCGCGGAGAACGTGTGGCTGGACATCTTCTTGAAG 1260  
QY 1270 GCCCTCAACTATGAGACCGGAGAGAGAAAGAGGCTATGATGTCAGAGCTGTGGT 1329  
DB 1261 GCCCTCAACTATGAGACCGGAGAGAGAAAGAGGCTATGATGTCAGAGCTGTGGT 1320  
QY 1330 GACATTGGGGGCGCAGATGGGCTTTTATCGGGGCGCAGGCTGTCACCATCTCGAGATC 1389  
DB 1321 GACATTGGGGGCGCAGATGGGCTTTTATCGGGGCGCAGGCTGTCACCATCTCGAGATC 1380  
QY 1390 CTAGACTACTCTGTGAGGTGTCCGAGACAAAGTCTGGGATATTTTCGGAACCGACAG 1449  
DB 1381 CTAGACTACTCTGTGAGGTGTCCGAGACAAAGTCTGGGATATTTTCGGAACCGACAG 1440  
QY 1450 CACTCCCAAGGCACTCCAGACCAATCTGCTTCAGGAAGGCTGGGCAAGCATCAAC 1509  
DB 1441 CACTCCCAAGGCACTCCAGACCAATCTGCTTCAGGAAGGCTGGGCAAGCATCAAC 1469  
QY 1510 CAAGTTCCCACTCAGGCTGGGCGCCAGACCTCCCAAGCCCTCTGTCGCTACCAAG 1569  
DB 1470 -----GACTCCCAAGCCCTCTGTCGCTACCAAG 1501  
QY 1570 ACTCTCTCGGCTCCAGCGCAGCAGCTGTACTCTGTGACACAGCTGAGACCTCTGTCTG 1629  
DB 1502 ACTCTCTCGGCTCCAGCGCAGCAGCTGTACTCTGTGACACAGCTGAGACCTCTGTCTG 1561  
QY 1630 TGTCTCTGAGAGCCCGGCTGAGATCCTGTGAGCAATGCTGACCTGACAGTGTCTTCCT 1689  
DB 1562 TGTCTCTGAGAGCCCGGCTGAGATCCTGTGAGCAATGCTGACCTGACAGTGTCTTCCT 1621  
QY 1690 CTTTACCCCAATTAAGTCTTAATGATCAAAAAA 1732  
DB 1622 CTTTACCCCAATTAAGTCTTAATGATCAAAAAA 1664  
RESULT 6  
AAV84190  
ID AAV84190 standard; cDNA to mRNA; 1711 BP.  
XX  
AC AAV84190;



XX 29-MAR-1999 (first entry)  
XX DE Sodium channel receptor hSLNAC1 homologous cDNA.  
XX KW hSLNAC1: sodium channel receptor; human; ds; cyclic; circular.  
OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 76..1632  
XX FT /\*tag= a  
XX MO9854316-A1.  
XX PD 03-DEC-1998.  
XX PE 15-MAY-1998; 98MO-EP02884.  
XX PR 30-MAY-1997; 97EP-0401196.  
XX PA (SYNO ) SYNTHELABO.  
XX PI Besnard F, Graham D, Renard S;  
XX DR WPI: 1999-070215/06.  
XX DR P-PSDB: AAM88251.  
XX PT A new sodium channel receptor - useful for, e.g. treatment of  
XX PT neuronal degenerate problems, Alzheimer's, Parkinson's disease and  
XX PT morphine dependence  
XX PS Claim 22: Page 37-40; 63pp: English.  
XX CC This cDNA sequence, derived from human cerebellum, shows homology  
XX CC to novel human sodium channel receptor hSLNAC1 polynucleotide (see  
XX CC AA084189), and hybridises under conditions useable for amplification  
XX CC or for use as a probe or marker. It codes for a 518-amino acid  
XX CC polypeptide (see AAM88251). hSLNAC1 (see also AAM88250) is a member of  
XX CC a new class of sodium channel proteins that may be responsible for  
XX CC some nervous system transmissions, or may be used as a target to  
XX CC regulate some transmissions linked to various pathologies.  
XX SQ Sequence 1711 BP; 329 A; 578 C; 481 G; 323 T; 0 other:  
Query Match 87.1%; Score 1508.2; DB 20; Length 1711;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 1582; Conservative 0; Mismatches 8; Indels 59; Gaps 1;  
OY 84 CAGCACTGCTCGATGACAGGGGCTGGGACGCTTTCGGGCCAGGACGCTGAGCCTGCG 143  
DB 63 CGGCACGAGCTCGATGACAGGGGCTGGGACGCTTTCGGGCCAGGACGCTGAGCCTGCG 122  
OY 144 CCGGGGATGTGGGAGGCGCGCTGTCTGTGCACTGGGCACTCTCTTACAGAGTGGC 203  
DB 123 CCGGGGATGTGGGAGGCGCGCTGTCTGTGCACTGGGCACTCTCTTACAGAGTGGC 182  
OY 204 TGAGAGGCTGGGCTACTACAGGAGTTCCACCACAGACTGGCTGGATGAGCAGAAAG 263  
DB 183 TGAGAGGCTGGGCTACTACAGGAGTTCCACCACAGACTGGCTGGATGAGCAGAAAG 242  
OY 264 CCACCGGCTGCTTCCGGGCTGTCACCTGTGCAACATCAACCCAGTCGCGGCTGCG 323  
DB 243 CCACCGGCTGCTTCCGGGCTGTCACCTGTGCAACATCAACCCAGTCGCGGCTGCG 302  
OY 324 CCTAACGCGCAACGACCTGCACTGGGCTGGGCTGCTGCTGGGCTGGATCCGCGAGA 383  
DB 303 CCTAACGCGCAACGACCTGCACTGGGCTGGGCTGCTGCTGGGCTGGATCCGCGAGA 362  
OY 384 GCAGCGCGCTTCTGCGCGCGCTGGGCGCGGCGCGCTGCACCGCGCGCTTCATGCGCAG 443  
DB 363 GCAGCGCGCTTCTGCGCGCGCTGGGCGCGGCGCGCTGCACCGCGCGCTTCATGCGCAG 422

OY 444 TCCACCTTTGACATGGCGCAACTATGCCCTGTGGGCACTCCCTGGATGACATGCT 503  
DB 423 TCCACCTTTGACATGGCGCAACTATGCCCTGTGGGCACTCCCTGGATGACATGCT 482  
OY 504 GCTGAGCTGCTTCCGGGCTGCAACCTTGGGGCTGAGACTTACACAGATCTTAC 563  
DB 483 GCTGAGCTGCTTCCGGGCTGCAACCTTGGGGCTGAGAACTTACACAGATCTTAC 542  
OY 564 CCGATGGGAAAGTCTACACATTTAACTTGGGCTGTATGGGCGAGAGCTGTCCACAC 623  
DB 543 CCGATGGGAAAGTCTACACATTTAACTTGGGCTGTATGGGCGAGAGCTGTCCACAC 602  
OY 624 TACTAGGGGTGCAATGGGCAATGGCTGGACATCATGCTGGACGTGACAGAGGAATA 683  
DB 603 TACTAGGGGTGCAATGGGCAATGGGCTGGACATCATGCTGGACGTGACAGAGGAATA 662  
OY 684 TCTACTGTTGTGGAGGAAATGAGAGAGCCGTTTGAAGTGGGGAATCCGATGACAGT 743  
DB 663 TCTACTGTTGTGGAGGAAATGAGAGAGCCGTTTGAAGTGGGGAATCCGATGACAGT 722  
OY 744 CCACAGCCAGAGAGAGCGCCCATCATGATGACGCTGGGCTTGGGCTTCCCGGCTA 803  
DB 723 CCACAGCCAGAGAGAGCGCCCATCATGATGACGCTGGGCTTGGGCTTCCCGGCTA 782  
OY 804 CCAGACCTTTGTTCTTGGCAGCAGCAGCAGTGAAGCTTCTGCGCACCGCCCTGGGCGA 863  
DB 783 CCAGACCTTTGTTCTTGGCAGCAGCAGCAGTGAAGCTTCTGCGCACCGCCCTGGGCGA 842  
OY 864 TTGCAATTCAGATCTGTGAAACCCCACTATGAGCAGACGCCCTGTGATCCCTGAGGCTC 923  
DB 843 TTGCAATTCAGATCTGTGAAACCCCACTATGAGCAGACGCCCTGTGATCCCTGAGGCTC 902  
OY 924 CCCCAGCCCAAGCCCAAGCCCTTCCCTATACCTTATGAGGCTGTGCGCTGGCGGAAC 983  
DB 903 CCCCAGCCCAAGCCCAAGCCCTTCCCTATACCTTATGAGGCTGTGCGCTGGCGGAAC 962  
OY 984 CCGTACGTGCTGTGGAAGTGGGCTGCCGAATGAGTATCATGCGAGCGAGTGGCCAGT 1043  
DB 963 CCGTACGTGCTGTGGAAGTGGGCTGCCGAATGAGTATCATGCGAGCGAGTGGCCAGT 1022  
OY 1044 GTGCAAGCCCAAGCAGTACAAAGAACTGTGCCACCGCCGCTATGATGCCATCTTCGGA 1103  
DB 1023 GTGCAAGCCCAAGCAGTACAAAGAACTGTGCCACCGCCGCTATGATGCCATCTTCGGA 1082  
OY 1104 GGACGTGTGGGCTGCCCAACCCCTGTGGCGCAGCAGCGGCTATGCGCAGAGAGCTTCAT 1163  
DB 1083 GGACGTGTGGGCTGCCCAACCCCTGTGGCGCAGCAGCGGCTATGCGCAGAGAGCTTCAT 1142  
OY 1164 GGTGCGGATCCCGAGCGCGCGCGCGCGCTTCTGTGCGCGGAAGCTCAACCGCAGCGA 1223  
DB 1143 GGTGCGGATCCCGAGCGCGCGCGCGCGCTTCTGTGCGCGGAAGCTCAACCGCAGCGA 1202  
OY 1224 GGCCTACATTCGGGGAAGAGTGTGGGCTGGGCACTCTTGTGAGGCTTCACTATGA 1283  
DB 1203 GGCCTACATTCGGGGAAGAGTGTGGGCTGGGCACTCTTGTGAGGCTTCACTATGA 1262  
OY 1284 GACCGTGGAGAGAAAGAGGCTATGAGATGTCAAGAGCTGTGGTGTGATTTGGGGCGCA 1343  
DB 1263 GACCGTGGAGAGAAAGAGGCTATGAGATGTCAAGAGCTGTGGTGTGATTTGGGGCGCA 1322  
OY 1344 GATGGGCTTTTTCATGGGGCGAGCTGTCTCAACATCTCTGAGATCTTACACTTCTGTG 1403  
DB 1323 GATGGGCTTTTTCATGGGGCGAGGCTGTCTCAACATCTCTGAGATCTTACACTTCTGTG 1382  
OY 1404 TGAGGTGTTCCGAGACAGAGTCTGGGATATTTCGTGGAACGACAGCACTCCCAAGGCA 1463  
DB 1383 TGAGGTGTTCCGAGACAGAGTCTGGGATATTTCGTGGAACGACAGCACTCCCAAGGCA 1442  
OY 1464 CTCACGACCAATCTGCTTACAGAAAGGCTGGGACGATGAACCCAAAGTTCGCCCACT 1523  
DB 1443 CTCACGACCAATCT----- 1457  
OY 1524 CAGCCTGGGCCCCAGACCTCCACCCCTCTCCTGTGCGGTACCAAGAACTCTTCGCGCTC 1583



Db 865 GATCCGACGACTTTGATTCAGAGCCCTCTGATCCCTTGGTTCCCGCAGACCC 924  
QY 940 AGCCCTCCCTATACCTTATGGGGTGTGCTGCGCTGAGCCCTGGAACCCCGCTAGCTGCTGG 999  
Db 925 AGCCCTCTTATAGTTTAATAGTTTGTGCTGCTGCTGCTGAGTCTCGCTATGTGCTGG 984  
QY 1000 AAGTGGGCTGCCGAGATGTTTACATGCGAGCGAGCTGCGAGTGTGAGCCCGCAGAG 1059  
Db 985 AAGTGTGGCTGTGAAATGATGATGCTGCTGGAACCTCCCGAGTGTGAGCCCGCAGAG 1044  
QY 1060 TACAAGAACTGTGCCCGCCCGCCATATAGTCCATCTCTCCGAGAGACTCGTGGCCCTGC 1119  
Db 1045 TACAAGAACTGTGCCCGCCCGCCATATAGTCCATCTCTCCGAGAGACTCGTGGCTGC 1104  
QY 1120 CCCAACCCGCTGCGCAGCAGCGCTACCGCAAGAGCTCTCCATGCTCGATGCCGATCCGAGC 1179  
Db 1105 CCCAACCCGCTGCGCTACCTACCTGCGCGGAATACAAACGAGAGTCTCTCATGTGCTGGATCC 1164  
QY 1180 CGCGCCGCGCGCGCTTCTGCGCGCGAGCTCAACCGCAGCGAGCCTACATCGCGAG 1239  
Db 1165 CGCGCTGAGCTGCTGCTACCTGCGCGGAATACAAACGAGAGTCTCTCATGTGCTGGATCC 1224  
QY 1240 AAGCTGTGCGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1299  
Db 1225 AATGTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1284  
QY 1300 AAGGCTGTGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1359  
Db 1285 GCGGCTGTGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1344  
QY 1360 GGGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1419  
Db 1345 GAGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404  
QY 1420 AAGGCTGTGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479  
Db 1405 AAGCTGTGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464  
QY 1480 CTTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1539  
Db 1465 CTTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1524  
QY 1540 CTTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1599  
Db 1525 CTTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1584  
QY 1600 CTTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617  
Db 1585 CTTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1602

RESULT 8  
AAZ61201  
ID AAZ61201 standard; cDNA; 1602 BP.  
XX  
AC AAZ61201;  
XX  
DT 30-MAY-2000 (first entry)  
XX  
DE cDNA encoding a rat acid-sensitive cationic channel 3 (rASIC3).  
XX  
KW Neuronal acid-sensitive cation channel; ASIC; ASIC 3;  
KW proton-gated cation channel; biphasic desensitisation; amiloride;  
KW cation transport channel; acid sensor; pH detection; ds.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT 1..1602  
FT CDS /\*tag- a  
FT /product= "acid-sensitive cationic channel 3"  
PN W0200008149-A2.

XX 17-FEB-2000.  
PD  
XX  
XX 05-AUG-1999; 99WO-IB01445.  
PF  
XX 05-AUG-1998; 98US-0095408.  
PR  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
PA  
XX  
XX Waldmann R, Bassilana F, Lazdunski M, De Welle JR;  
PI WPI: 2000-195574/17.  
DR P-PSDB; AAY69179.  
XX  
XX Novel human cation transport protein, Acid Sensing Ionic Channel 3 used  
PT to identify substances capable of modulating cation transport channel  
PT activity -  
XX  
XX Disclosure; Page 77-79; 84pp; English.  
XX  
XX The present sequence encodes a rat neuronal acid-sensitive cation  
CC channel 3 (ASIC3) protein. The protein is a proton-gated cation  
CC channel subunit that has biphasic desensitisation kinetics with both  
CC a rapidly inactivating sodium-selective and a sustained component. The  
CC channels are sensitive to amiloride. The specification describes ASIC3  
CC proteins, which are expressed in the sensory neurons but not in the  
CC brain. The cation transport channel proteins can be used in methods to  
CC identify substances capable of modulating the activity of cation  
CC transport channels. The human ASIC3 protein is also an acid sensor,  
CC and might play an important role in the detection of lasting pH changes  
CC in humans.  
XX  
SQ Sequence 1602 BP; 328 A; 498 C; 434 G; 342 T; 0 other;

Query Match 63.3%; Score 1096.4; DB 21; Length 1602;  
Best Local Similarity 81.2%; Pred. No. 1.6e-232;  
Matches 1282; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

QY 43 GAGAGAGCCCGGAGCCCTGCGAGATCGCGCTGTTCCGACCACTGCTGATGAC 102  
Db 25 GAGGCCCCAGGCGGACAGGCTGAGACATCGGGTGTTCGACACAGCTGCAATCAT 84  
QY 103 GGGCTGGGCGACGTTTCGCGGCGAGCACTGAGCTGCGCGCGGGGAGATGCGCAGCG 162  
Db 85 GGTGTGGGCGACATCTTGGGCGTGGAGGCTGACCTCGCGCCAGGCGTGTGGGCGACA 144  
QY 163 GCGTGGGCTGCTGAGGCGGACCTTCCTACAGGAGGCTGAGAGGCTGCTGCTACTAC 222  
Db 145 GCTGTGCTCTGTGCTGCGCTGCGGCTTCTCTACAGGTGCTGAGCGGCTTCTGCTACTAT 204  
QY 223 AGGAGTTCCACACAGACTGCTGCTGATGAGCGAGAAAGCCACCGCTGCTTCCG 282  
Db 205 GGGGAGTTCCACCAATTAAGACACCTGATGAGCGTGAAGCCACGACCTTCCCA 264  
QY 283 GCTGTACCTGTGCAACATTAACCACTGCGCGCTGCGGCTTAACGCCCAAGCACTG 342  
Db 265 GCTGTGACTGTGTAAATATCAACCACTGCGCGCTGACGCCCAACCAAGCACTG 324  
QY 343 CACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 402  
Db 325 CACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384  
QY 403 GCGCTGGGCGGCGGCGGCTGACCGCGGCTTCAATGCGCACTGCGCACTTGTGACATGGC 462  
Db 385 GCACTGGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444  
QY 463 CAACTGTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522  
Db 445 CAACTGTATGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504  
QY 523 GCGCAACCTGTGCGGCTGAGAACTTACCAACGACTTCAACCGGAGGGAAGTGTAC 582  
Db 505 GCGCAGCGCTGTGGGCTGAGAACTTCAACGATGATCTTACTGAAATGGGCAATGCTAC 564

QY	583	ACATTTAACTCTGGCGGTATGGGGGACAGAGCTGTACACACTACTAGAGGGGTGGCATGGGG	642
Db	565	ACCTTCAACTCTGTGTGCCACGGGTGCAGAGCTCTTACCACCTCCAAAGGGTGTCTGTGGC	624
QY	643	AATGGGCTGGACATCATGCTGTGAGCGTGCAGCAGAGAGGAATATCTACTGTGTGGAGGAC	702
Db	625	AACGCACTAGAGATTAATGTCTAGATGTATACAGCAAGAGAGATTAATCTGCCATCTGGAAGAC	684
QY	703	AATAGAGAGACCCCGTTTGAAGGTGGGGATTCAGAGTGCAAATCCACAGCCAGAGAGAGCCG	762
Db	685	ATTGAAAGAGACCCCGTTTGAAGGTGGGGATTCAGAGTGCAAATTCACAGCCAGGATTAAGCC	744
QY	763	CCCAATCTCATAGCTAGCTGGGGCTTGGGGGGTGTCCCGGGCTTACAGACCTTTGTCTTGC	822
Db	745	CTGTGCATTAACAGAGCTGGGGCTTGGGGGGACGCCAGGCGATCAAGCTTTGTGTCTGT	804
QY	823	CAGCAGACAGACGCTGAGCTCTTCGCCACCGCGCTGGGGCGATTGCAAGTTCAAGATCTGTG	882
Db	805	CAGCAGAGAGAACTGAATTTTCTGTGCACACACCTGGGGGTAGCTGGAATACCCATCTTGG	864
QY	883	AATCCCAACTA --- TGAAGCAGAGACCCCTGTGATCCCTTGAAGCTCCCGCCAGCCAGCC	939
Db	865	GATCCGACGACCTTTGATTCAGAGCCCTCTGATCCCTTGGTGTCCCGACAGCCAGACCC	924
QY	940	AGCCCTCCCTAATACCTTTATGGGGTGTGGCTGTGGCTGGGAAACCCGGTACGTGGCTGG	999
Db	925	AGCCCTCCCTAATAGTTAATAGGTTGTGGCTGTGGCTGTGGATCTGCAATGTGGCTGG	984
QY	1000	AATGGGCGCTGGCGAATGGGTATCATGCCAGAGCGAGAGTGCACAGTGTGCAGCCGCCACAG	1055
Db	985	AATGTGTGCTGTGCATAGATGATGCATATGGCTGGAAATCCCTCCAGTGTGCAGCCCCACAG	1044
QY	1060	TATCAAGAACTGTGGCCACCCGGGCATATGATGTGCATCTTTCGGAAGAGACTGTGCAGCTGC	1119
Db	1045	TACAAAGACTGTGGCCACCCAGCTGTGAAGCGTATCTGTGAAAGAGACAGCTGTCTTGC	1104
QY	1120	CCCAACCCGTGGCCAGCAGCGCTTACGCCAGAGAGCTCTCATGTGTGGATCCCGAGC	1179
Db	1105	CCCAACCCGTGGCGCTACTATACAGCTATATGCCAAGAGACTCTCATGTGTGGGATTCACAGC	1164
QY	1180	CGGCGCGCGGGCGCTTCCGTGGGCGCGGAAGCTCAACCGAGAGAGGCGCTTACATGGCGGAG	1233
Db	1165	CGCGCTGTACGTGCTTACTCTGGCCCGGAAATPACAAACCGAGGAGTCTTACTATTAAGGGAG	1222
QY	1240	AACGTGTGGCGCTGTGACATCTTCTTTGAAGGCCCTCACTATGAGACCTGTGAGCAGAG	1295
Db	1225	AATGTACTGGTTTGTGATATCTTCTTTGAGGCCCTCACTATGAAAGCGGTGTGACAAAG	1288
QY	1300	AAGGCTATAGATGTGAGAGCTGTGGTGTGACATTTGGGGCCAGATGGGCTTTTTCATC	1355
Db	1285	GGCGGCTATGAAGTGTGGAGCTGTGGGAGACATTTGGGGGACAGATGTGGGACTGTTTATT	1344
QY	1360	GGGGCAGGCGGCTCACCATCTCTGAGAGCTGTAGACTACTCTGTGTAGGTGTTCGAGAGC	1419
Db	1345	GGAGCAAGGCTGCTTACCATCTCTGTGAGATCTGTGACTATCTCTGTGAGTTTTCAGAGAC	1404
QY	1420	AAGGTCTGGGATATTTTCTGAAACGAGACGACTCCCAAGGCACTCCAGACCAATCTG	1479
Db	1405	AGAATCTGGGGATTTTCTGGAACAGAGAGGCGCTCAAAAGGCGCTGTGGCAACACTGTG	1466
QY	1480	CTTGAGGAAGGGCTGGGGCAGCCATTCAGACCCAGTTCCCACTCTAGCGCTGGGGCCCGAGA	1533
Db	1465	CTCAGGAAGAGTGAATGGCATTCGAACCAATGTTTCCCACTCTAGCCTTAAGGGCCAGG	1522
QY	1540	CTTCCCAACCCCTCCCTGTGGCGTACACAGAGACTCTCTCCGCTCCCAACGCACTGTCTAC	1595
Db	1525	CTCTCTTACCACTCTCTGTGTGTACACAGACACTCTTGCGCTCCCACTGTACGTGTTCAC	1588
QY	1600	CTTGTACACAGCTCTTGA 1617	
Db	1585	CTGTCTACAAAGGCTCTTGA 1602	

AS17128	standard; cDNA, 1602 BP.
AA17128	
AA17128	
14-FEB-2002	(first entry)
Rat cDNA encoding acid sensing ion channel subunit 3, ASIC3A.	
Rat; ss; acid sensing ion channel, ASIC3A; analgesic; anti-HTV; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; cerebroprotective; cardiatic; antitanginal; hypotensive; antiatherosclerotic; vasotropic; tranquiliser; antidepressant; chronic pain; neuropathic pain; diabetes; cancer; AIDS; acquired immunodeficiency syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Creutzfeldt-Jacob disease; amyotrophic lateral sclerosis; dementia; convulsion; epilepsy; stroke; anxiety; depression; angina; cardiovascular disease; congestive heart failure; vasoconstriction; hypertension; atherosclerosis; restenosis; bleeding; gene therapy.	
Rattus sp.	
Key	Location/Qualifiers
CDS	154..1692
	/tag= a
	/product= "ASIC3A"
WO200181570-A2.	
01-NOV-2001.	
20-APR-2001; 2001WO-CA00561.	
20-APR-2000; 2000CA-2304494.	
(UWMC-) UNIV MCGILL.	
Seguela P, Babiniski K;	
WPI; 2002-055353/07.	
P-PSDB; AAU10906.	
New heteromultimeric proton-gated ion channel for diagnosing, treating diseases associated with expression of the channel e.g. neurodegenerative diseases, comprises two different types of acid sensing ion channel subunits	
Claim 7; Page 100-101; 105pp; English.	
The invention relates to a protein complex forming a heteromultimeric amiloride- and gadolinium-sensitive proton-gated cation channel (ASIC-2S.2), where the individual components of the heteromultimeric channel include the acid sensing ion channel (ASIC2A and ASIC3 protein or their variants having 80% sequence identity, the channel being activated by protons, acids, low pH solutions, the nucleic acids encoding the subunits, a recombinant bicistronic vector comprising a nucleic acid encoding at least two individual subunits or variants of ASIC-2S.2, a host cell comprising the vector, an antibody raised against one of the subunits or a domain which is capable of disrupting assembly of the ion channel and antagonists of the ion channel. The polypeptides and polynucleotides are useful for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the heteromultimeric channel (e.g. by gene therapy using the vector). Such diseases include chronic pain, neuropathic pain such as diabetic-, cancer- and AIDS (acquired immunodeficiency syndrome)-related, neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease, Huntington's disease, Creutzfeldt-Jacob disease, and amyotrophic lateral sclerosis and dementias, including AIDS-related as well as convulsions, epilepsy, stroke, anxiety and depression. They are also useful for treating cardiovascular diseases such as angina, congestive	

CC heart failure, vasoconstriction, hypertension, atherosclerosis,  
 CC renoemosis and bleeding. ASIC-2s.2 plays a role in the regulation of  
 CC neurotransmitter release. ASIC-2s.2 plays a role in the regulation of  
 CC useful in screening for compounds that regulate neurotransmitter release,  
 CC synaptic efficacy, neuroexcitability or neurotoxicity. The present  
 CC sequence encodes rat ASIC3A.

XX Sequence 1602 BP; 328 A; 498 C; 434 G; 342 T; 0 other:

Query Match 63.38; Score 1096.4; DB 24; Length 1602;  
 Best Local Similarity 81.28; Pred. No. 1,6e-232;  
 Matches 1282; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

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QY 43 GAGAGGCCCGGCGGAGCCCTCGGACATCCGCGGTTCGCGAGCAGTGCATGCATGCAC 102
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 25 GAGGCCCGGCGGCGGAGCCCTCGGACATCCGCGGTTCGCGAGCAGTGCATGCATGCAT 84
QY 103 GGGCTGGGCGGAGCTTCCTGGGCGGAGCCCTGAGCCCTGGCCCGGGGATGTGGCGACG 162
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85 GGTCTGGGCGGAGCTTCCTGGGCGGAGCCCTGAGCCCTGGCCCGGGGATGTGGCGACG 144
QY 163 GCGCTGGCTTCGAGTGGGCGGAGCCCTCTCTACAGTGGCTGAGAGGGTGGCTACTAC 222
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 145 GCTGTGCTCTGTGGTGGGCGGCTTCCTCTACAGTGGCTGAGAGGGTGGCTACTAT 204
QY 223 AGGAGTTCACACAGAGACTGCGCTGGATGAGCGAGAAAGCCACCGGCTGCTTCCG 282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 205 GGGGAGTTCACACAGAGACTGCGCTGGATGAGCGAGAAAGCCACCGTCACTTCCCA 264
QY 283 GCTGTACCTCTGTGCATACATACCCACTGCGCGCTGCGCTTCAGCCCGCAAGACTG 342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 265 GCTGTACCTCTGTGTAAATACACCCACTGCGCGCTGCGCTTCAGCCCGCAAGACTG 324
QY 343 CACTGGGCTGGTGGCTGCTGCTGAGGCTGATCCCGGAGAGACGCGGCTTCTGCGC 402
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Db 325 CACTGGGCTGGAGAGGCTGCTGCTGAGGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 384
QY 403 GCGCTGGGCGGCGGCGGCTGACCGCGCGCTTCATGCGCAATGCCCTTTGAGATGGCG 462
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 385 GCACTGGGCGGCGGCGGCGGCTGACCGCGCTTCATGCGCAATGCCCTTTGAGATGGCA 444
QY 463 CAATCTATGCGCGCTGCTGCGGCTGCTGCTGATGATGATGCTGCTGCTGCTGCTGCT 522
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 CAATCTATGCGCGGCTGCTGCGGCTGCTGCTGATGATGATGCTGCTGCTGCTGCTGCT 504
QY 523 GCGCAACCTTGTGGGCGCTGAGAACTTCACAGATCTTCACCGGATGGAGAAAGTGTAC 582
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 GCGCAACCTTGTGGGCGCTGAGAACTTCACAGATCTTCACCGGATGGAGAAAGTGTAC 564
QY 583 ACATTTAACTTGGCGCTGATGGGCGAGAGCTGCTACACCACTACTAGGGGTGCATGGGC 642
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 ACCTTCAACTTGTGGCGGCTGAGAGAGCTGCTACCACTCAAAAGGGTGGTGGC 624
QY 643 AATGGGCGGAGATCATGCTGAGTGGAGAGAGAAATTCATGCTGTGAGAGGAC 702
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 625 AATGGGCGGAGATCATGCTGAGTGGAGAGAGAAATTCATGCTGTGAGAGGAC 684
QY 703 AATGAGGAGACCCGCTTTGAGAGTGGGATCGAGTGCATGCACAGCGCAGAGAGCGG 762
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 685 ATGGAAGAGACCCGCTTTGAGAGTGGGATCGAGTGCATGCACAGCGCAGAGAGAGCGG 744
QY 763 CCATTCATCATGAGCTGGGCTTGGGGGTGTCCCGGGCTACAGAGCTTTTGTCTTTC 822
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 CCTGCCATTCAGCAGCTGGGCTTGGGGGACAGCCCGAGCCATCAGACTTTTGTGTCTGT 804
QY 823 CAGAGAGAGAGCTGAGCTTCTGCGACCGCTGGGCGCATTCAGATTCAGCATCTCTG 882
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 805 CAGAGAGAGAGCTGAGCTTCTGCGACCGCTGGGCGCATTCAGATTCAGCATCTCTG 864
QY 883 AACCCCAACTA--TGAGCGAGAGCCCTGATCCCTAGGCTGCCAGCGCCAGCGCCC 939
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 865 GATCCGACGACTTTGATCCAGAGCCCTGTGATCCCTTGGGTCCCGCAGACCGACGCC 924

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QY 940 AGCCCTCCCTATACCTTATGAGGAGTGGCTGGCTGGCTGCGAAGCCGCTAGCTGGCTGG 999
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 925 AGCCCTCCCTATAGTTTAATAGTTTGGCTGGCTGGCTGGCTGCTAGCTAGCTGGCTGG 984
QY 1000 AAGTGGCTCCGAAATGTGTACATCCAGCGAGCGAGCTGCCAGTGTGACGCCCGCAGCAG 1059
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 985 AAGTGGCTCCGAAATGTGTACATCCAGCGAGCGAGCTGCCAGTGTGACGCCCGCAGCAG 1044
QY 1060 TACAAGATGCTGGCCGAGCCGATAGATCCATCCCTTGGGAGAGCTGGGCTGGC 1119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1045 TACAAGATGCTGGCCGAGCCGATAGATCCATCCCTTGGGAGAGCTGGGCTGGC 1104
QY 1120 CCCAAGCCGCTGGCGAGCGAGCGCTACGCCAAGAGAGCTTCATAGTGGAGATCCCGAGC 1179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 CCCAAGCCGCTGGCGAGCGAGCGCTACGCCAAGAGAGCTTCATAGTGGAGATCCCGAGC 1164
QY 1180 GCGGCGCGCGCGCTTCTGCGCGGAGAGCTCAACCGCAGCGAGCCCTACATGCGGAG 1239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1165 GCGGCGCTGAGCTGCTGCTGCTGCGCGGAGAGCTCAACCGCAGCGAGCTTACATTCAGGAG 1224
QY 1240 AAGCTGCTGGCGCTGGAGATCTCTTGGAGGCGCTCAACTATGAGACCGTGGAGCAGAG 1299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1225 AATGCTACTGTTCTGGATATCTTCTTGGAGGCGCTCAACTATGAGAGCGGTGGAACAAAG 1284
QY 1300 AAGGCTATGAGATGTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
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Db 1285 GCGGCTATGAGATGTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344
QY 1360 GGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1345 GAGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1404
QY 1420 AAGTCTCTGGGATATTTCTGGAACCGAGCTGCCAAGAGCGCTGCGAGCACTATCTG 1479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1405 AGATGCTCTGGGATATTTCTGGAACCGAGCTGCCAAGAGCGCTGCGAGCACTATCTG 1464
QY 1480 CTTCAGAGAGGCTGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1465 CTTCAGAGAGGCTGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1524
QY 1540 CTTCCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1525 CTTCCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1584
QY 1600 CTTCGACACAGCTCTAG 1617
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1585 CTTCGACACAGCTCTAG 1602

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RESULT 10  
 AAX28161  
 ID AAX28161 standard; cDNA to mRNA; 2962 BP.  
 XX  
 AC AAX28161;  
 DT 16-JUN-1999 (first entry)  
 XX  
 DE Rat Acid sensitive ion channel coding sequence.  
 XX  
 KW Acid sensitive ion channel: rat; ASIC; pH mediated pain disorder;  
 KW Ischaemia; gene therapy; proton-gated ion channel; ds.  
 XX  
 OS Rattus sp.  
 PN W09911784-A1.  
 XX  
 XX 11-MAR-1999.  
 XX  
 PF 28-AUG-1998; 98MO-GB02609.  
 PR 29-AUG-1997; 97GB-0018365.  
 XX  
 PA (UNLO ) UNIV COLLEGE LONDON.

XX Akopian AN, Chen C, England S, Wood JN;  
 XX WPI: 1999-205188/17.  
 DR P-PSDB; AA03186.  
 XX  
 PT Acid sensitive ion channel (ASIC) proteins - useful in gene therapy  
 PT for treatment of pH mediated pain disorders  
 XX  
 PS Claim 7: Page 43-47; 62pp; English.  
 CC This sequence encodes an acid sensitive ion channel (ASIC) of the  
 CC invention, isolated from rat dorsal root ganglion. Antisense ASIC DNA or  
 CC RNA is useful in gene therapy for downgrading expression of ASIC protein,  
 CC for pH mediated pain disorders e.g. in ischemia. The vectors are useful  
 CC for incorporating ASIC DNA or RNA for use in gene therapy. Proton-gated  
 CC ion channel agonists and antagonists are identified using cells  
 CC transfected with ASIC DNA by allowing interaction between the candidate  
 CC substance and ASIC protein in the membrane, and measuring interaction  
 CC and/or cell response. Partial agonists and antagonists can be identified  
 CC by their ability to block the response of the cell to present in a  
 CC solution of a given acid pH or any agonist. The hybridisation probes are  
 CC useful for screening libraries for ASIC DNA or RNA.  
 CC  
 SQ Sequence 2362 BP; 655 A; 850 C; 785 G; 672 T; 0 other;  
 Query Match 27.3%; Score 472.2; DB 20; Length 2962;  
 Best Local Similarity 59.0%; Pred. No. 1e-94;  
 Matches 925; Conservative 0; Mismatches 578; Indels 66; Gaps 4;

5 ACACGCGGTTTGGCCATGAGCCCACTCAGGCCAGAGAGGCCGCGGAGCCCT 64  
 191 AAGAGGAG 250  
 65 CGGACATCCGCGTGTTCGCGCAGCACTCTCATGAGAGAGAGAGAGAGAGAG 124  
 251 GGGAGTTGGTGGCTTGGCCAGCAGCTGACCTCATGAGAGAGAGAGAGAGAG 310  
 125 CAGGACGCTGAG 184  
 311 AAGGAGGAG 370  
 185 CTTCTCTTACAG 244  
 371 CTTCTCTTACAG 430  
 245 CCGTGTATGAG 304  
 431 TGTAG 490  
 305 ACCCACTGCGCGCGCTGCGCGCTAAGCCCAAGACCTGAGAGAGAGAGAGAG 364  
 491 ATCCCGCTGCGCGCTGCGCGCTAAGCCCAAGACCTGAGAGAGAGAGAGAG 547  
 365 TGGGCTGAGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424  
 548 TAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595  
 425 CGCGCGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484  
 596 GCCAGAGAGCTTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655  
 485 ACTTCCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544  
 656 ACCGCTGAG 715  
 545 ACTTACACAGATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604  
 716 ACTTCTCAG 775  
 605 GGGCAG 664  
 776 GGGGCGACAG 835

665 ACGTCAGAGAGAGATATCTACCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 724  
 836 ACATTCAGAGAGAGATATATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 895  
 725 TGGGATCCGAG 784  
 896 CAGAGATCAAG 955  
 785 TGGGAGTGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844  
 956 TTGGT 1015  
 845 TGGCAGCGGAG 904  
 1016 TGCCCTTACCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1064  
 905 CTTCTGATCCCTTACCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964  
 1065 -----CTTCAGACTCTACAGATCAGTCCCT 1090  
 965 GTGGCTGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1024  
 1091 GCGGATTTGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150  
 1025 TGGCAGGCGAG 1084  
 1151 TGGCAGGCGAG 1210  
 1085 TAGATGCAATCTCT-----TGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1138  
 1211 TGGATCTCTTGT 1270  
 1139 CCGGCTAGCGCAG 1198  
 1271 CCGGCTAGCGCAG 1330  
 1199 TGGCAGGCGAG 1258  
 1331 TGGCAGGCGAG 1390  
 1259 TCTTCTTGTGAG 1318  
 1391 TTTTCTTGTGAG 1450  
 1319 AGCTGTTGTGAG 1378  
 1451 GCGTGTGTGTGAG 1510  
 1379 TCCCTGAG 1438  
 1511 TGTGTGAG 1570  
 1439 GGAACGAG 1498  
 1571 AGTGTGAG 1630  
 1499 GCGATGAG 1558  
 1631 ACGTCAAG 1690  
 1559 CCGTCAG 1657  
 1691 CTGCGAG 1699

RESULT 11  
 AAV60842  
 ID AAV60842 standard; DNA: 3647 BP.  
 AC AAV60842;  
 XX  
 DT 02-FEB-1999 (first entry)





Db 1370 TGSCAAGAAGTTCACAAATCGAGCATACATAGAGGAGAGAAATTCGTGTGACAA 1429  
 QY 1259 TCTTCTTGAGGCCCTCACTATGAGACCTGGAGCAGAAAGGCTATGAGATGTCAG 1318  
 Db 1430 TTTTCTTTGAAGCTTCACATATGAGACCAATCGAGAGAAAGGCTATGAGATGTCAG 1489  
 QY 1319 AGCTGCTGGTGCATTTGGGCGAGATGGGCTTTTTCATCGGGGCCAGCTGTGCACCA 1378  
 Db 1490 GCGTGTGGGTGCATCGGAGGCGGAGATGGGCTTTTCATCGGTCGACATCTCACC 1549  
 QY 1379 TCTCTGAGATCTTACAGTACCTCTGTGAGGTCTTCCGAGACAAGTCTTGATATTTCT 1438  
 Db 1550 TGTGTGAAGCTTTGACTATGCTAGAGAGTCAATTAAGCAGAGGCTGTGACAGCTGGA 1609  
 QY 1439 GGAAGCAGACGACTCCCAAGGACATCCAGCACCATCTGCTTCAGGAAGGCTGGCA 1498  
 Db 1610 AGTGCAGAAAGGAGGTAAAGAGAGACGACAGCAAGGCGCTGCGCTCAGCTGGATG 1669  
 QY 1499 GCGATGAAACCAAGTTCCCGACCTGAGCTGGGCGCCAGACCTGCCACCCCTGCTGTG 1558  
 Db 1670 AGCTCAAAAGACACAAATCCCTCGAGAGCTCCGAGAGACATCCTGCCGGATGACGAC 1729  
 QY 1559 CCGTCAACA 1567  
 Db 1730 CTGCCAACA 1738  
 RESULT 12  
 AA61200  
 ID AA61200 standard; cDNA; 3647 BP.  
 XX  
 AC AA61200;  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE cDNA encoding a rat acid-sensitive cationic channel 1B (rASIC1B).  
 XX  
 DE Neuronal acid-sensitive cation channel; ASIC; ASIC 1B;  
 KM proton-gated cation channel; biphasic desensitisation; amiloride;  
 KM cation transport channel; acid sensor; pH detection; ds.  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 109..1788  
 FT /tag= "a  
 FT /product= "acid-sensitive cationic channel 1B"  
 XX  
 PN WO200008149-A2.  
 XX  
 PD 17-FEB-2000.  
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 PF 05-AUG-1999; 99WO-IB01445.  
 XX  
 PR 05-AUG-1998; 98US-0095408.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Waldmann R, Bassilana F, Lazdunski M, De Weille JR;  
 DR WPI: 2000-195574/17.  
 DR P-PSDB; AAY69178.  
 XX  
 PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used  
 PT to identify substances capable of modulating cation transport channel  
 PT activity  
 XX  
 PS Disclosure: Page 73-76; 84p; English.  
 XX  
 CC The present sequence encodes a rat neuronal acid-sensitive cation  
 CC channel 1B (ASIC1B) protein. The protein is a proton-gated cation  
 CC channel subunit that has biphasic desensitisation kinetics with both  
 CC a rapidly inactivating sodium-selective and a sustained component. The

CC channels are sensitive to amiloride. The specification describes ASIC3  
 CC proteins, which are expressed in the sensory neurons but not in the  
 CC brain. The cation transport channel proteins can be used in methods to  
 CC identify substances capable of modulating the activity of cation  
 CC transport channels. The human ASIC3 protein is also an acid sensor,  
 CC and might play an important role in the detection of lasting pH changes  
 CC in humans.  
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 SQ Sequence 3647 BP; 895 A; 853 C; 900 G; 999 T; 0 other;  
 Query Match 27.2%; Score 470.6; DB 21; Length 3647;  
 Best Local Similarity 58.9%; Pred. No. 2.4e-94;  
 Matches 924; Conservative 0; Mismatches 579; Indels 66; Gaps 4;  
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 Db 290 GGGACTTGTGGCTTCTGCGCAACAGCTTACCTTTCATGGTCCAGCATGTGTTGTGG 349  
 QY 125 CAGGACACTGAGCCTGCGCGCGGAGATGGGCGAGCGCGTGTCTGTCACTGGCCA 184  
 Db 350 AAGGGGCCCAAGGCCCAAGGCAAGGCTTATGGCAGAGTGGCTTGTATAGCACTGGGTG 409  
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 Db 410 CTTTCTTCTGACAGGTGAGGAGGAGCGCGTGTCTTATATACCTACCACTACCACTG 469  
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QY 1025 TGCCAGGAGCGTGGCAGTGTCCAGCCCGCAGCATACAGAAAGTGGCCCGCGGCGCA 1084
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Db 1730 CTGCCACA 1738

RESULT 13
AAV60840
ID AAV60840 standard; DNA: 1620 BP.
XX
AC AAV60840;
XX
DT 02-FEB-1999 (first entry)
XX
DE Partial human acid sensing ionic channel gene.
XX
KW Human: neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
KW acid sensing ionic channel; hybridization; primer; PCR; amplification;
KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
KW amyotrophic lateral sclerosis; cerebellar ataxia; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1545
FT /*tag= a
FT /product= "partial ASIC"

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FT /note= "acid sensing ionic channel; no start codon
FT is given at the 5' end of the sequence"
PN MO9835034-A1.
PD 13-AUG-1998.
XX
PF 11-FEB-1998; 98WO-FR00270.
XX
PR 28-JUL-1997; 97FR-0009587.
PR 11-FEB-1997; 97FR-0001574.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M,
PI Waldmann R, Lingueglia E;
DR WPI: 1998-447231/38.
DR P-PSDB; AAW68505.
XX
PT Protein comprising proton-sensitive neuronal channel - useful for
PT screening for analgesics and for treating neurodegeneration
PS Claim 13: Page 28-30; 64pp; French.
XX
CC This sequence represents a partial gene encoding a human neuronal
CC cationic channel that is sensitive to amiloride and activated by protons
CC and is designated Acid Sensing Ionic Channel (ASIC). The protein can be
CC used to screen for modulators of these channels, particularly to identify
CC compounds that modulate perception of acidity, as regards nociception
CC (pain) rather than taste. These compounds are used to treat or prevent
CC pain associated with acidity (e.g. in cases of inflammation, ischaemia
CC or some tumours) and as inhibitors of neurodegeneration caused by
CC overexpression of the channels. Antibodies to the protein are used to
CC detect the channels in tissues, and to act therapeutically as channel
CC modulators. The nucleic acid can be used to generate transgenic,
CC particularly knockout, animals for studying ASIC-related disorders,
CC also for gene therapy. The channel protein, or its (ant)agonists, can
CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.
CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
CC sclerosis or cerebellar ataxia).
XX
SO Sequence 1620 BP; 372 A; 470 C; 465 G; 313 T; 0 other;

Query Match 26.4%; Score 456.8; DB 19; Length 1620;
Best Local Similarity 58.5%; Pred. No. 2.2e-91;
Matches 893; Conservative 0; Mismatches 567; Indels 66; Gaps 3;

QY 69 CATCCGCGTGTTCGCCAGCAACTGCTGATGCAGCGGCTGGGCCACGTCTTGCGGCCAG 128
Db 9 CATCCAGGCTTTCGCCAGCAGCTCCACATGACAGGATGGCCACATCTCTCTTACGA 68
QY 129 CAGCTGAGCTGCGCGCGGGGATGTGGGACAGCGCCGTGTGCTGTAGTGGCACCTT 188
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QY 364 -----CTGGGCTGTGATCCCGAGAGACCGCGCTTCTGCGCGCCT 407
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QY 648 GTTGACATCATGCTGAGAGCTGACAGCAGAGAGAATATCTACCTGTGTGAGGACATGA 707
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QY 768 CATCATCAGCTGGGCTTGGGGGTGTCCCGGGCTACAGACCTTGTCTTCCAGCA 827
Db 729 CATGCACAGCTGGGCTTGGGGTGTCCCGGGCTTCCAGACCTTGTGTGGCTGCCAGGA 788
QY 828 GCAGCAGCTGACCTTCTCTCCACCGCCCTGGGGCGATGACAGTCTGTGAACCC 887
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QY 888 CAAGTATGAGCCAGAGCCCTGTGATCCCTAGGCTCCCGAGCCCGAGCCCTCC 947
Db 849 GGATTTGGATTTCTTCGACT-----C 869
QY 948 CTATACCTTATGGGGTGTGCGCTGCGTGCAGAAACCGCTACGCTGCGAATGCCG 1007
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QY 1008 CTGCGCAATGCTGATCATGCTGAGGCGAGCTGCCAGTGTGAGCGCCAGCAGTCAAGAA 1067
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RESULT 14
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ID AAZ61198 standard; cDNA; 1620 BP.
XX
AC AAZ61198;
XX
DT 30-MAY-2000 (first entry)
DE
DE cDNA encoding a partial acid-sensitive cationic channel 1A (ASIC1A).
XX
XX Neuronal acid-sensitive cation channel; ASIC; ASIC 1A;
XX proton-gated cation channel; biphasic desensitisation; amiloride;
XX cation transport channel; acid sensor; pH detection; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1545
XX FT /tag= a
XX FT /product= "partial acid-sensitive cationic channel 1A"
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XX WO200008149-A2.
XX
XX 17-FEB-2000.
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XX 05-AUG-1999; 99WO-1B01445.
XX
XX 05-AUG-1998; 98US-0095408.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Waldmann R, Bassilana F, Lazdunski M, De Weille JR;
XX WPI; 2000-195574/17.
XX DR P-PSDB; AAY69176.
XX
XX Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
XX to identify substances capable of modulating cation transport channel
XX activity.
XX
XX Disclosure; Page 67-69; 84pp; English.
XX
XX PS The present sequence encodes a human partial neuronal acid-sensitive
XX cation channel 1A (ASIC1A) protein. The protein is a proton-gated cation
XX channel subunit that has biphasic desensitisation kinetics with both
XX a rapidly inactivating sodium-selective and a sustained component. The
XX channels are sensitive to amiloride. The specification describes ASIC3
XX proteins, which are expressed in the sensory neurons but not in the
XX brain. The cation transport channel proteins can be used in methods to
XX identify substances capable of modulating the activity of cation
XX transport channels. The human ASIC3 protein is also an acid sensor,
XX and might play an important role in the detection of lasting pH changes
XX in humans.
XX
XX SO Sequence 1620 BP; 372 A; 470 C; 465 G; 313 T; 0 other;
Query Match 26.4%; Score 456.8; DB 21; Length 1620;
Best Local Similarity 58.5%; Pred. No. 2..2e-91;
Matches 893; Conservative 0; Mismatches 567; Indels 66; Gaps 3;
QY 69 CATCCGCTGTGGCCAGCAAGCTCGATGCACGGGCTGGCCAGCTTGGGGCAGG 128
Db 9 CATCCAGGCTTGCACGACGCTCCACACTGCACGGGATGGCCACATCTTCTTACGA 68
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 ID AAV60839 standard; DNA: 3562 BP.  
 XX  
 AC AAV60839;  
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 DT 02-FEB-1999 (first entry)  
 XX  
 DE Rat acid sensing ionic channel ASIC1A gene.  
 XX  
 KW Rat: neuronal cationic channel; amiloride; proton; ASIC; brain; probe;  
 KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;  
 KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;  
 KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;  
 KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;  
 KW anyotropic lateral sclerosis; cerebellar ataxia; ds.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 123..1703  
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 FT /product= "ASIC1A"  
 FT /note= "acid sensing ionic channel 1A"  
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 XX MO9835034-A1.  
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 XX PD 13-AUG-1998.  
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 XX PF 11-FEB-1998: 98WO-FR00270.  
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 XX PR 28-JUL-1997: 97FR-0009587.  
 XX PR 11-FEB-1997: 97FR-0001574.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M;  
 PI Waldmann R, Lingueglia E;  
 XX  
 DR WPI: 1998-447231/38.  
 DR P-PSDB: AAW68504.  
 XX  
 PT Protein comprising proton-sensitive neuronal channel - useful for  
 PT screening for analgesics and for treating neurodegeneration  
 XX  
 PS Claim 12: Page 24-27; 64pp; French.  
 XX

CC This sequence represents the gene encoding a rat neuronal cationic  
CC channel that is sensitive to amiloride and activated by protons and  
CC is designated Acid Sensing Ionic Channel (ASIC). This sequence  
CC represents the rat ASIC1a gene. The sequence was isolated from a rat  
CC brain DNA library using a probe amplified by primers AAV0845-760846.  
CC The protein can be used to screen for modulators of these channels,  
CC particularly to identify compounds that modulate perception of acidity,  
CC as regards nociception (pain) rather than taste. These compounds are  
CC used to treat or prevent pain associated with acidity (e.g. in cases of  
CC inflammation, ischaemia or some tumours) and as inhibitors of  
CC neurodegeneration caused by overexpression of the channels. Antibodies  
CC to the protein are used to detect the channels in tissues, and to act  
CC therapeutically as channel modulators. The nucleic acid can be used to  
CC generate transgenic, particularly knockout, animals for studying  
CC ASIC-related disorders, also for gene therapy. The channel protein,  
CC or its (ant)agonists, can be used to treat or prevent cerebral  
CC neurodegenerative conditions (e.g. Alzheimer's, Parkinson's or  
CC Huntington's diseases, amyotrophic lateral sclerosis or cerebellar  
CC ataxia).

SQ Sequence 3562 BP; 905 A; 827 C; 862 G; 968 T; 0 other;

Query Match	26.28;	Score 453.2;	DB 19;	Length 3562;
Post Total Cnt/Match	50.18	Post Max Cnt	15.00	

Match	Best Local Similarity	Best Local Similarity P-Value	Match	Mismatches	Indels	Gaps
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Db	147	GAGGGGGGTGGATGTCACACCCGGTAGACATCCAGGCTTTCCGACAGCACTCCACAGCTGAT	206
OY	103	GAGGCTGGGCGCACAGTCCTGGGGCGACGGACCTGAGCCCTGGGCGGGGGGATGTGGGCGAGC	162
Db	207	GGTCTTGCCCACTTCCTTCTCTTAGAGCGGCTGTCTCTTGAAGCGGGCACTGTGGCCCTG	266
OY	163	GCCGTGTCCTGTAGTGGGCCACCTTCTCTTACACAGGTGGCTGAGAGGGGTGGCTGTATAC	222
Db	267	TGCTTCCTGGGGTGTGGCTGGCGGCTCTGCTGTGTGTGACACTAGAGCGCTGTGCACTATAC	326
OY	223	AGGAGTTCACACACACAGACTGCTCCCTGGATGAGCGAGAAAACCACGGCTGTCTTCGG	282
Db	327	TTTCTGCTATCCACACAGTCACCAACCTTGACAGAACTGGCTGCTCCACCTTCCCT	386
OY	283	GCTGTACCCGTGCACATACCAACCACTGGCGGCTTCGGCCCTAAGGCCAAGACCTG	342
Db	387	GCTGTACACGTGTGCAACTCTCAATGAGTTCGCTTTAGCCAAAGCTCCAAGAAATGACCTG	446
OY	343	CACCTGGCTGGGTCGAGCTG-----CTGGGCTGATATCCCGCA	381
Db	447	TACCATGCTGGGAGACTGCTGCCCCCTGTCAACAACAGATATAGATATCCGGACACACAG	506
OY	382	GAGCACGCGCGCTTCCTGCGCGCCCTGGGCGCGCCCTCGACCCGCGCGCTTCATGCC	441
Db	507	ATGGCTGATGAAAAGACACTAGAGATATGGAGAGCAAGGCAACTTCCGGAGCTTCAG	566
OY	442	AGTCCCACTTTGACATGCGCAACTATATGCCGTGTGGGCACTCCCTGATGACATG	501
Db	567	CCCAAGCCCTTCAACATGCTGAAATTTACACAGACAGCGGGCGACGATATTCAGACATG	626
OY	502	CTGCGGACCTGCGGTCCGTTCCGGGCGCAACCTGTGGGGCTGAGAACTCACACAGATCTC	561
Db	627	CTGCTCTGTGCGCACTTCCGTGGGGAAGGCTGTGACCGCTTGAAGATTTCAAGTGTCTTC	686
OY	562	ACCCCGATGGGAAAGTCTTACACATTTTAACCTGAGCGCTGTATGGGCGAGAGTGCCTACC	621
Db	687	ACTGGGTATGGGAAGTGTACCACTTCAACTCGGGCCCAACTGGGCGGCCACGCGCTAAG	746
OY	622	ACTACTAGGGTGGCATGGGCAATGGCGTGACATCATGTGACGTCAGACAGAGAA	681
Db	747	ACCAATGAAGGTGGGACTGCGCAATGGCGCTGAGATCATGTGCGACATTTACGAAGAATGAA	806
OY	682	TATCTACTGTGTGGAGGGACAATGAGAGAACCCCGTTTAGAGTGGGGATCCAGTGCAG	741
Db	807	TATTTGCTGTGTGGGAGAACCGACAGACATCTTTCGAAGCGAGCATTAAGTCTCAG	866

QY	742	ATTACAGCCAGAGAGAGGCGCCGCAATCATGCAGCTGGGCTTGCGGGGTGTCGCCGGCC	801
Db	867	ATCCACAGTCAGAGTAAGACCCCTTCATCTAGACACACTGGCTTGGTGTGGCTCCACGT	926
QY	802	TACCAGACCTTTGTTCTTCTCCAGCAGCAGCAGCTAGCTTCTCTCCACCGGCTGGGGC	861
Db	927	TTCCAGACGTTTGTGTCTTGTCCAGAGAGAGAGGCTATCTTACTGCGCCACACCTGGGGC	986
QY	862	GATTGCACTTACAGCATCTCTGAACCCCACTATAGCCAGACCCCTTGATCCCTTAGGC	921
Db	987	ACCTGCAATGCTGTATTACCAATGAGACTGGAGATT-----	1018
QY	922	TCGCCAGCCCCACCGACCCCTCCCTATACCTTATGGGCTGCTGGCTGCAGAA	981
Db	1019	-----CTTCGACTCTTACAGCATATCACTGCTGCCGAGATTGATTTGGAG	1061
QY	982	ACCCGCTACGTGCTCGGAAGTGGCGGCTGCCGAGTGGTACATGCGCAGCGAGCTGCCA	1041
Db	1062	ACGGGTATACCTGGTGGAGAACTCAACTGCGCTATGGTACATGCGCAGAGGGAGCCCCA	1121
QY	1042	GTTGGACGCCCCCGACGATCAGAAAGCTGTGGCCACCGCGCATATGATCCATTCCT----	1097
Db	1122	TACTGCACTCCAGACAGTACAAAGAGGTGCGAGATCTGCTCGTGACTTCTTAATGGAG	1181
QY	1098	--TGGCAGAGCACTGTGCGGCTGCGCCCAACCCCTGGCGCCAGCAGCGGCTTACCCCAAGAG	1155
Db	1182	AAAGCAGAGGAAATCTGCTGTTGTGAGATGCTTTGGACACTGACCCGCTAGCGCAAGGAG	1241
QY	1156	CTTCTCATGTGGTGGGATCCGAGCCGCGCGCGCGCTTCTGTGGCCGGAACTCAAC	1215
Db	1242	CTGTTCATAGGTCAAGAAATCCCAAGCAAAAGCTCCGCCAAATACTGTGGCCAAAGAAATTCAAC	1301
QY	1216	CGCAGCGAGGCTCTATCTCGGCGGAGAAAGTCTGGCCCTGGACATCTCTTTAAGGCCCTC	1275
Db	1302	AAATCGAGCACTACATAGGGGAGAAACATTTCTGTGTGACATTTTCTTTAAAGTCTTC	1361
QY	1276	AACTATGAGACCCGTGAGCAGAAAGAGCCCTATGAGATGTCAAGAGCTGCTTGATCAATT	1335
Db	1362	AACTATGAGACCATTCAGAGCAAGAAAGAGCCCTATGAGATGTCAAGAGCTGCTTGATCAATT	1421
QY	1336	GGGGGACAGATGGGCTTTTTCATCTGGGGCCAGCGCTGCTACCACTCTCGAGATCCTAAGC	1399
Db	1422	GGGGGACAGATGGGGTGTTCATCTGGGCGCAGAGATCCTCAACGCTGTGTGAATCTTTTGAAC	1481
QY	1366	TACCTCTGTGAGGTTCCTCCAGACAAAGTCTCTGGATATTCTTGGAAACGACAGCATCC	1455
Db	1482	TATGCTCTACGAGGTTCATTTAAGCAGAGGCTGTGAGACGTGGAAAGTGGCCAGAAAGGAGCT	1541
QY	1456	CAAAAGCACTTCAGACACCAATCTGCTTCAAGAAAGGCTGGGCAAGCCATCGAAACCAAGTT	1515
Db	1542	AAAGAGACACCGCAGACAAAGAGGCGTGGCGCTCAGCCTGGATGACGTCAAAAGACACAAT	1601
QY	1516	CCCCACCTCAAGGCTGGGCCCCAGACCTCCACCCCTCTCTGTGGCTGACCA	1567
Db	1602	CCCTCGAGACCTTCGAGAGCATCTGCGCGGATGACAGCTGCTGCACAA	1653

Search completed: October 11, 2002, 02:52:12  
Job time : 296 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 02:44:14 : Search time 1943 Seconds  
(without alignments)  
12051.254 Million cell updates/sec

Title: US-09-530-233-1

Perfect score: 1732  
Sequence: 1 tgcacagacgcgtctgc.....tgcatacaaaaaaaaaa 1732

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estlov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.2	33.2	580	9	AL046680 DKFZp434B
2	524	30.3	594	10	BM352497 1967e03.x
3	467	27.0	503	9	AM770119 h183h06.x
4	445.6	25.7	452	9	AA884721 am19a09.s
5	439.4	25.4	584	10	BG895217 358498 MA
6	429.2	24.8	498	10	BF344753 602014005
7	415.6	24.0	422	9	A1580095 tk16c11.x
8	401	23.2	429	9	AA449322 zx06e07.s
9	386.8	22.3	469	9	A1684829 wa86b06.x
10	357	20.6	579	9	AM742291 up55b10.y
11	353	20.4	564	9	A1179632 ESR223356
12	342	19.7	342	9	AA448259 z983e12.s
13	335.2	19.4	1059	10	BG825318 602747771
14	326.8	18.9	503	9	A1024055 ov72c01.s
15	325.6	18.8	835	10	B1548575 603189513
16	321.4	18.6	778	10	B1697646 603348823
17	309	17.8	890	9	AL534267 AL534267

c	18	307.4	17.7	552	9	A1556742	UI-R-C2p-
	19	305.2	17.6	343	9	AA449579	AA449579 zx06e07.r
	20	299.2	17.3	447	10	BF547366	BF547366 UI-R-C2p-
	21	297.8	17.2	378	9	AA628357	AA628357 ag02d03.s
	22	293.2	16.9	318	9	A1337738	A1337738 gw92c06.x
	23	291.4	16.8	483	10	B1683443	B1683443 464831 MA
	24	291	16.8	379	9	AA428361	AA428361 zw51e10.s
	25	287.4	16.6	522	9	BE120172	BE120172 UI-R-CAO-
	26	283	16.3	324	10	BF885304	BF885304 RC6-TN007
	27	282.2	16.3	470	9	AM743006	AM743006 up55b10.x
	28	278.6	16.1	482	10	B1294094	B1294094 UI-R-DK0-
	29	277	16.0	470	10	BM352813	BM352813 1967e03.y
	30	272.6	15.7	290	9	A1188057	A1188057 ge14e02.x
	31	265.8	15.3	667	10	BG912912	BG912912 602807309
	32	258.2	14.9	293	9	A1859572	A1859572 wml3g02.x
	33	253.8	14.7	444	10	BF460933	BF460933 UI-M-CG0p
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	35	233.4	13.5	527	10	B1342038	B1342038 369690 MA
	36	231.8	13.4	571	10	B1342335	B1342335 370074 MA
	37	226	13.0	539	9	A1425640	A1425640 md59d07.y
	38	197	11.4	825	10	B1731397	B1731397 603353854
	39	194.2	11.2	669	9	AV225999	AV225999 AV225999
	40	190.4	11.0	812	10	BG818664	BG818664 602778855
	41	188.4	10.9	786	10	B1823745	B1823745 603040868
	42	188	10.9	509	10	BF514399	BF514399 UI-H-BW1-
	43	185.8	10.7	457	9	AM444547	AM444547 UI-H-B13-
	44	183.8	10.6	534	9	A1567447	A1567447 tn38d03.x
	45	183.8	10.6	823	10	B1734817	B1734817 603356691

#### ALIGNMENTS

RESULT 1  
AL046680  
LOCUS  
DEFINITION DKFZp434B219\_r1 434 (synonym: htes3) Homo sapiens cDNA clone  
DKFZp434B219 5', mRNA sequence.

ACCESSION AL046680.1 GI:5434743

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 580)  
Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
EST (Poustka, et al.)  
Unpublished (1999)  
Contact: Poustka A.J.  
Department Lehnach  
Max-Planck-Institute for Molecular Genetics  
Innestrasse 73, 14195 Berlin, Germany  
Tel: +49-30-84131623  
Fax: +49-30-84131128  
Email: poustka@mpg-berlin-dahlem.mpg.de  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp434B219) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubergweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
location/Qualifiers  
1. 580  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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#### FEATURES

source



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/dev_stage="adult"
/lab_host="DH10B"
/Note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
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Best Local Similarity 99.5%; Pred. No. 7.9e-99;
Matches 577; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Oy 1062 CAAGAAGCTGTGCCCCACCCGGCATAGATGCCATCTTGGCAAGAGACTGTGGCGCTGCC 1121
Db 1 CAAGAAGCTGTGCCCCACCCGGCATAGATGCCATGCTTGGCAAGAGACTGTGGCGCTGCC 60
Oy 1122 CAACCGTGTGCGCAGCAGCGCGCTACGCCAAGAGAGCTTCATGGTGGGATCCGAGCG 1181
Db 61 CAACCGTGTGCGCAGCAGCGCGCTACGCCAAGAGAGCTTCATGGTGGGATCCGAGCG 120
Oy 1182 GCGCGCGCGCGCTTCCTGGCCCGGAGCTCAACCGCAGCGCGCTACATCGCGAGAA 1241
Db 121 GCGCGCGCGCGCTTCCTGGCCCGGAGCTCAACCGCAGCGCGCTACATCGCGAGAA 180
Oy 1242 CGTGTGCGCGCTGACATCTTCTTGGAGCCCTCAACTATGAGACCGTGGAGCAAGAA 1301
Db 181 CGTGTGCGCGCTGACATCTTCTTGGAGCCCTCAACTATGAGACCGTGGAGCAAGAA 240
Oy 1302 GCGCATAGATAGTACAGAGCTGTGTGACATTTGGGGGCGCATGGGCTTTTCATCG 1361
Db 241 GCGCATAGATAGTACAGAGCTGTGTGACATTTGGGGGCGCATGGGCTTTTCATCG 300
Oy 1362 GCGCAGCGCTGCTCACCATCTCTGAGATCTTACCTCTGTGTGAGTGTTCGAGCAA 1421
Db 301 GCGCAGCGCTGCTCACCATCTCTGAGATCTTACCTCTGTGTGAGTGTTCGAGCAA 360
Oy 1422 GGTCTGTGATATTTCTGGAACCGCAGCAGCTCCCAAGGACCTCCAGCAGCAATCTCT 1481
Db 361 GGTCTGTGATATTTCTGGAACCGCAGCAGCTCCCAAGGACCTCCAGCAGCAATCTCT 420
Oy 1482 TCAGGAAGGGCTGGGCGACCATCGAACCAAGTTCCCGCAGCTGAGGCGCCGAGAC 1541
Db 421 TCAGGAAGGGCTGGGCGACCATCGAACCAAGTTCCCGCAGCTGAGGCGCCGAGAC 480
Oy 1542 TCCCAACCCCTCTGTGTGCGGTACCAAGATCTCTCCGCTCCAGCGCAGCTGTA 1601
Db 481 TCCCAACCCCTCTGTGTGCGGTACCAAGATCTCTCCGCTCCAGCGCAGCTGTA 540
Oy 1602 TGTCAACAGCTAGACCTGCTGTCTGTCTGTGAGC 1641
Db 541 TGTCAACAGCTAGACCTGCTGTCTGTCTGTGAGC 580

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RESULT 2
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LOCUS      1667e03 x1 HR85 1slet Homo sapiens cDNA 3' similar to TR:Q0URH4
DEFINITION      Q0URH4 ACID SENSING ION CHANNEL 3 SPLICE VARIANT B.; mRNA
sequence.
ACCESSION      BM352497
VERSION        BM352497.1 GI:18084855
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      Melton,D., Brown,J., Kenly,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishke,I., Scarse,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Maira,M., Pape,D., Wylie,T., Martin,J., Bilstain,A.,
Schmitt,A., Theising,B., Ritey,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
TITLE      Endocrine Pancreas Consortium
JOURNAL      Unpublished (2000)

```

```

COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@lohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -400p from Glibco
High quality sequence stop: 383.
location/Qualifiers
1. 594
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/db_xref="taxon:9606"
/clone_id="HR85 1slet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/Note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

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BASE COUNT      116 a      154 c      198 g      126 t
ORIGIN

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Query Match      30.3%; Score 524; DB 10; Length 594;
Best Local Similarity 94.5%; Pred. No. 3.6e-89;
Matches 554; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

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Db 586 GCGTACGCCAAGAGAGCTCTCCATGTGTGCGGATCCGAGCGCGCGCGCGCTTC 527
Oy 1198 CTGCGCGCGAAGCTCAACCGCAGCGAGGCTTACATCGCGGAGAACCTGTGCGCTGAC 1257
Db 526 CTGCGCGCGAAGCTCAACCGCAGCGAGGCTTACATCGCGGAGAACCTGTGCGCTGAC 467
Oy 1258 ATCTTCTTGAAGCGCTCAACTATAGACCGTGAAGCAGAGAAGCGCTATAGATGTCA 1317
Db 466 ATCTTCTTGAAGCGCTCAACTATAGACCGTGAAGCAGAGAAGCGCTATAGATGTCA 407
Oy 1318 GAGCTGCTGTGACATTTGGGGCCAGATGGGCTTTTCATCGGGGCCAGCTCTGAC 1377
Db 406 GAGCTGCTGTGACATTTGGGGCCAGATGGGCTTTTCATCGGGGCCAGCTCTGAC 347
Oy 1378 ATCCCGAGATCTTACACTCTCTGAGAGGTGTTCCGAGCAAGGTCCTGGATATTTC 1457
Db 346 ATCCCGAGATCTTACACTCTCTGAGAGGTGTTCCGAGCAAGGTCCTGGATATTTC 287
Oy 1438 TGAACGAGCAGACCTCCCAAGGACACTCGACACCAATCTGCTTCAAGAGGCGTGGG 1497
Db 286 TGAACGAGCAGACCTCCCAAGGACACTCGACACCAATCTGCTTCAAGAGGCGTGGG 227
Oy 1498 AGCCATGACCAAGATTTCCCGACCTGAGCTGGGCGCCGAGACCTCCACCCCTGCT 1557
Db 226 AAAATATGAACCAAGATTTCCCGACCTGAGCTGGGCGCCGAGACCTCCACCCCTGCT 167
Oy 1558 GCGGTACCAAGACTCTCTCGGCTCCACCGCAGCAGCTGCTTGTACACACCTAG 1617
Db 166 GCGGTACCAAGACTCTCTCGGCTCCACCGCAGCAGCTGCTTGTGTACACACCTAG 107
Oy 1618 ACCTGCTGTCTGCTCTCGGAGCGCGCGCTGACATCTGAGACATGCTAGCTGACG 1677
Db 106 ACCTGCTGTCTGCTCTCGGAGCGCGCGCTGACATCTGAGACATGCTAGCTGACG 47

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AM770119/c			
LOCUS			
DEFINITION	AM770119	503 bp	mRNA
	h183h06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone		linear
	IMAGE:2978939 3 similar to TR:035240 035240 PROTON GATED CATION		EST 04-MAY-2000
CHANNEL DRASIC.	:		mRNA sequence.
AM770119			
AM770119.1	GI:7702158		
EST.			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 503)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from GlDco High quality sequence stop: 457. Location/Qualifiers		
FEATURES			
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	/clone="IMAGE:2978939"		
	/clone_id="Soares_NFL_T_GBC_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-GCAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The diveren was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."		
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Matches 487;	Conservative 0;	Mismatches 16;	Indels 1;
		Gaps	1;
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OY	1279	TATGAGACCCTGGAGACAAGAAGGCCCTATGAGATGTAGAGCTGCTTGAGCATTTGGG	1338
Db	443	TATGAGACCCTGGAGACAAGAAGGCCCTATGAGATGTAGAGCTGCTTGAGCATTTGGG	384
OY	1339	GCCCGATGGGGCTTTTATCGGGGGCCAGCGCTGCACATCCCTCGAGTCCCTAAGTAC	1398
Db	383	GCCCGATGGGGCTTTTATCGGGGGCCAGCGCTGCCTCACCATCTCTGAGATCTTAGACTTAC	324
OY	1399	CTCTGTGAGGTGTTCCGAGACAAGGTCTCTGGGATATTTCTTGGAACCGACACTCCAA	1458
Db	323	CTCTGTGAGGTGTTCCGAGACAAGGTCTCTGGGATATTTCTTGGAACCGACACTCCAA	264
OY	1459	AGGCATCTCAGACACAATCTGTTAGAGAAGGCTGGGCGACGATCGAACCAGATTCCC	1518

Db	Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Comment	Features
Db	263	AGGCATCTCAGACCAACAACTCGTTTCAGGAAAGGCGTGGGACAGCAATCGAAGCCAAAGTTGCC	204							
Db	1519	CACCTCAGCCTTGGGCCCCAGACCTCCACACCCCTCCCTGTGCGCTGACCAAGACTCTTCC	1578							
Db	203	CCCCCAGACGCTGGGGCCCCAGACCTCCACACCCCTCCCTGTGCGCTGACCAAGACTCTTCC	145							
Db	1579	GGCTCCACCGGACCTGTCTTACCTGTGTACACAGGCTGTGACCTGTGTCTGTGTCTGTG	1638							
Db	144	GGCTCCACCGGACCTGTCTTACCTGTGTACACAGGCTGTGACCTGTGTCTGTGTCTGTG	85							
Db	1639	AGCCCCGCGCTGACATCTGTGACATGCTTACGCTGACAGTGTGCTTCCGCTTCCACCC	1698							
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Db	24	AAATTAAGTCTTAATGATCAAAA	1722							
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DEFINITION	am19a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone									
DEFINITION	IMAGE:1467256.3' similar to TR:035240 035240 PROTON GATED CATION									
DEFINITION	CHANNEL DRASIC. ; mRNA sequence.									
ACCESSION	AA884721									
VERSION	AA884721.1	GI:2994702								
KEYWORDS	EST.									
SOURCE	human.									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
TITLE	1 (bases 1 to 452)									
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.									
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),									
FEATURES	Tumor Gene Index									
SOURCE	Unpublished (1997)									
FEATURES	Contact: Robert Strausberg, Ph.D.									
FEATURES	Email: c9apbs@email.nih.gov									
FEATURES	This clone is available royalty-free through LNL; contact the									
FEATURES	IMAGE Consortium (info@image.llnl.gov) for further information.									
FEATURES	Possible reversed clone: similarity on wrong strand									
FEATURES	Insert Length: 1150 Std Error: 0.00									
FEATURES	Seq primer: -40ml3 fwd. ET from Amer sham									
FEATURES	High quality sequence stop: 134.									
FEATURES	Location/Qualifiers									
FEATURES	1. 452									
FEATURES	/organism="Homo sapiens"									
FEATURES	/db_xref="taxon:9606"									
FEATURES	/clone="IMAGE:1467256"									
FEATURES	/clone_id="Soares_NFL_T_GBC_S1"									
FEATURES	/lab_host="DH10B"									
FEATURES	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with									
FEATURES	a modified polylinker; Site:1: Not I; Site:2: Eco RI;									
FEATURES	Equal amounts of plasmid DNA from three normalized									
FEATURES	libraries (fetal lung NBHL19w, testis NT, and B-cell									
FEATURES	NCI-GAP GCBI) were mixed, and ss circles were made in									
FEATURES	vitro. Following HAP purification, this DNA was used as									
FEATURES	tracer in a subtractive hybridization reaction. The driver									
FEATURES	was PCR-amplified cDNAs from pools of 5,000 clones made									
FEATURES	from the same 3 libraries. The pools consisted of									

Db 452 GCCCTCACTATGAGACCGCTGAGACAGAGAGCCCTATGAGATCCAGAGCTGCTTGGT 393  
 QY 1330 GACATTGGGGGCGCAGATGGGCTTTTCATCGGGGCGAGCCGTCACACTCCTCGAGATC 1389  
 Db 392 GACATTGGGGGCGCAGATGGGCTTTTCATCGGGGCGAGCCGTCACACTCCTCGAGATC 333  
 QY 1390 CTAGACTACCTCTGTGAGGTGTTCGAGACAGAGTCTGGGATATATTTCTGAGACCGAG 1449  
 Db 332 CTAGACTACCTCTGTGAGGTGTTCGAGACAGAGTCTGGGATATATTTCTGAGACCGAG 273  
 QY 1450 CACTCCCAAGAGCAGCTCCAGACCAATCTGCTTAGAGAGGGCTGGGCGACCATCGAAC 1509  
 Db 272 CACTCCCAAGAGCAGCTCCAGACCAATCTGCTTAGAGAGGGCTGGGCGACCATCGAAC 213  
 QY 1510 CAAGTTCCCAAGCAGCTCCAGAGCCAGACCTCCCTGCTGGCGTCCAGAG 1569  
 Db 212 CAAGTTCCCAAGCAGCTCCAGAGCCAGACCTCCCTGCTGGCGTCCAGAG 153  
 QY 1570 ACTCTCGGCGCTCCAGCGACCTGCTACCTGTCTACAGAGCTTAGACCTGCTGTG 1629  
 Db 152 ACTCTCGGCGCTCCAGCGACCTGCTACCTGTCTACAGAGCTTAGACCTGCTGTG 93  
 QY 1630 TGTCTCGGAGCGCGGCTGACATCTGAGACAGTCTAGCTGAGCTGCTTTCCT 1689  
 Db 92 TGTCTCGGAGCGCGGCTGACATCTGAGACAGTCTAGCTGAGCTGCTTTCCT 33  
 QY 1690 CTTCACCCCAATTAAGTCTTAATGATCAAA 1721  
 Db 32 CTTCACCCCAATTAAGTCTTAATGATCAAA 1

RESULT 5  
 BG895217 584 bp mRNA linear EST 05-JUN-2001  
 LOCUS 358498 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.  
 DEFINITION BG895217  
 ACCESSION BG895217  
 VERSION BG895217.1 GI:14305458  
 KEYWORDS EST.  
 SOURCE pig.  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 584)  
 Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,  
 Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Laegreid, W.W.  
 and Keele, J.W.  
 Design and use of two pooled tissue normalized cDNA libraries for  
 EST discovery in swine  
 Unpublished (2000)  
 CONTACT: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred  
 v0.980904.e. Vector identified by cross-match with the -minscore 18  
 and -mismatch 12 options.  
 PCR Primers  
 FORWARD: AGGAAGACGCTATGACCAT  
 BACKWARD: GTTTTCCAGTCACGACG  
 PLACE: 121 row: A column: 15  
 Seq primer: ATTTAGTGACACTATAG.  
 Location/Qualifiers  
 1..584

## FEATURES

source  
 /organism="Sus scrofa"  
 /db\_xref="taxon:9623"  
 /clone\_lib="MARC 1Pig"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPOR6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from day 11, 13, 15, 20,  
 and 30 embryos."

BASE COUNT 104 a 195 c 173 g 112 t  
 ORIGIN

Query Match 25.4%; Score 439.4; DB 10; Length 584;  
 Best Local Similarity 85.9%; Pred. No. 3.4e-73;  
 Matches 501; Conservative 0; Mismatches 76; Indels 6; Gaps 1;

QY 866 GCAGTTCAGCATCTGGAACCCCAAGATAGAGCAGAGCCCTGTGATCCCTAGGCTGCC 925  
 Db 1 GCAGTTCATCTGTGACCTTGAGACCTTGACTTTGAGCCAGAACCTTGATCTTGCTGGCTTT 60  
 QY 926 CCAGCCCGACGCC-----AGCCCTCCATATACCTTATGGGGTTCGCTGGCTGG 979  
 Db 61 CCAGTCCAGCCCGGTCGCCAAGCCCTCCATATCTTAATGGGGTTCGCTGGCTGGC 120  
 QY 980 AATCCCGTACGTGGCTGGGAATGGGGCGTCCGATGGGTGATACATGCCAGGAGAGTGC 1039  
 Db 121 AGACTGCTTTGTGACCTGGGAATGGGGCTGGCGAATGATGATATGCTTGGCTGGCGCGCG 180  
 QY 1040 CAGTGTGACAGCCCGCAGAGTACAGAACTGTGCCACCCGCGCATATGATGATCTTC 1099  
 Db 181 CAGTGTGACAGCCCGCAGAGTACAGAACTGTGCCACCCGCGCATATGATGATCTTC 240  
 QY 1100 GCAGGACTGTGCGCTGCGTCCCAACCCGTGCGCAGACAGCGGCTACGCCAAGAGCTCT 1159  
 Db 241 GCGAGGAGCGTGTGACCTGCGCCCAACCCGTGCGCAGACAGCGGCTACGCCAAGAGCTCT 300  
 QY 1160 CCATGGTGGGATCCGAGCGCGCGCGGCGGCTTCCGTGGCGGGAAGCTCAACCGCA 1219  
 Db 301 CCATGGTGGGATCCGAGCGCGCGCGGCGGCTTCCGTGGCGGGAAGCTCAACCGCA 360  
 QY 1220 GCGAGGCTTACATCGCGGAGAAAGTGTCTGCGCTGAGCATCTTCTTGGAGCCCTCACT 1279  
 Db 361 GCGAGGCTTACATCGAGGAGAAAGTGTCTGAGTGTGACATCTTCTTGGAGCCCTCACT 420  
 QY 1280 ATAGACCGTGGAGCGAAGAAAGGCTTATGATGTGTCAAGCTGCTTGGTGTGATTTGGG 1339  
 Db 421 ACAGACGCGTGGAGCGAAGAAAGGCTTATGATGTGTGTGCGAGCTGTGAGGGGAG 480  
 QY 1340 GCCAGTGGGCGCTTTCATCGGGGGCGAGCGCTGTCACATCTCGATCTAGACTTAC 1399  
 Db 481 GCCAGTGGGCGCTTTCATCGGGGGCGAGCGCTGTCACATCTCGATCTAGACTTAC 540  
 QY 1400 TCTGTAGGTGTTCGAGACAAAGTCTTGGATATTTCTGGAA 1442  
 Db 541 TCTGTAGGTGTTCGAGACAAAGTCTTGGATATTTCTGGAA 583

RESULT 6  
 BF344753 498 bp mRNA linear EST 22-NOV-2000  
 LOCUS 602014005F1 NCI CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4149960  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BF344753  
 KEYWORDS BF344753.1 GI:11292199  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 498)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMU at:  
 http://lmage.llnl.gov

REFERENCE 1  
 AUTHORS NIH-MGC  
 TITLE NIH-MGC  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMU at:  
 http://lmage.llnl.gov

Plate: LLMW9412 row: 1 column: 01  
High quality sequence stop: 485.  
Location/Qualifiers  
1. 498

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4149960"  
/clone\_1lb="NCI\_CGAP\_Brn64"  
/tissue\_type="gliblastoma with EGFR amplification"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: Brain; Vector: pCMV-Sport6; Site\_1: Not I; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 112 a 171 c 114 g 101 t  
ORIGIN

Query Match 24.8%; Score 429.2; DB 10; Length 498;  
Best Local Similarity 95.2%; Pred. No. 2.8e-71;  
Matches 461; Conservative 0; Mismatches 3; Indels 20; Gaps 1;

QY 1269 GGGCCCTCAACTATGACACCGTGGAGCAGAAAGGCTATGAGATGTACAGCTGCTTGG 1328  
|||||  
DB 12 GGGCCCTCAACTATGACACCGTGGAGCAGAAAGGCTATGAGATGTACAGCTGCTTGG 71  
QY 1329 TGACATTTGGGGGCGACATGGGCTTTTCATCGGGGGCGAGCTGTCACCATCTCGAGAT 1388  
|||||  
DB 72 TGACATTTGGGGGCGACATGGGCTTTTCATCGGGGGCGAGCTGTCACCATCTCGAGAT 131  
QY 1389 CCTAGACTACCTCTGTGAGGTGTTCGAGACAGAGTCTGGATATTTCTGGAACCGACA 1448  
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DB 132 CCTAGACTACCTCTGTGAGGTGTTCGAGACAGAGTCTGGATATTTCTGGAACCGACA 191

QY 1449 GCACCTCCCAAGGACATCCAGACCAATCTGCTTCAAGAAAGGCTGGCAGCATGTAAC 1508  
|||||  
DB 192 GCACCTCCCAAGGACATCCAGACCAATCTGCTTCAAGAAAGGCTGGCAGCATGTAAC 251

QY 1509 CCNAGTTCGCCACCTCAGCTGGGGCCCC-----AGACCTCCACAC 1548  
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DB 252 CCNAGTTCGCCACCTCAGCTGGGGCCCCAGACCTGCTGTGTCCGAAGACCTCCACAC 311

QY 1549 CCTCCCTGTGGCGTCAACAAGACTCTCCGCCCTCCACGCACTGCTACCTTGTACAA 1608  
|||||  
DB 312 CCTCCCTGTGGCGTCAACAAGACTCTCCGCCCTCCACGCACTGCTACCTTGTACAA 371

QY 1609 CAGCTTTAAGCTGTGTGTCTGTGGAGGCGCGCTGACATCTGGAGATGCTTA 1668  
|||||  
DB 372 CAGCTTTAAGCTGTGTGTCTGTGGAGGCGCGCTGACATCTGGAGATGCTTA 431

QY 1669 GCCTGACGTAAGCTTTCCGCTTTCACCCCAATAAAGTCTTAATGCATCAAAAAAAA 1728  
|||||  
DB 432 GCCTGACGTAAGCTTTCCGCTTTCACCCCAATAAAGTCTTAATGCATCAAAAAAAA 491

QY 1729 AAAA 1732  
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DB 492 AAAA 495

RESULT 7  
A1580095/c 422 bp mRNA linear EST 13-DEC-1999  
LOCUS tk1611.x1 Soares.NHMPu.S1 Homo sapiens cDNA clone IMAGE:2151188  
DEFINITION 3' similar to TR:035240 O35240 PROTON GATED CATION CHANNEL DNASTIC.  
; mRNA sequence.

ACCESSION A1580095 GI:4564471  
VERSION A1580095.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 422)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Insert length: 493 Std Error: 0.00  
Seq primer: -40UP from Gibco  
POLYA-NO.

FEATURES  
source  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2151188"  
/clone\_1lb="Soares.NHMPu.S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pT7n3D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NDHM, pregnant uterus  
NBHPU, and fetal heart NBH19W) were mixed, and ss circles  
were made in vitro. Following NBP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

BASE COUNT 89 a 97 c 151 g 85 t  
ORIGIN

Query Match 24.0%; Score 415.6; DB 9; Length 422;  
Best Local Similarity 99.1%; Pred. No. 1e-68;  
Matches 418; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1302 GGGCTTNGAGATGTCAGAGTGTGTTGATTTGGGGGCGAATGGGCTTTTCATCGG 1361  
|||||  
DB 422 GGGCTTNGAGATGTCAGAGTGTGTTGATTTGGGGGCGAATGGGCTTTTCATCGG 363

QY 1362 GGGCAGCTGTGTCACCATCTCGAGATCTAGACTCTGTGAGGTGTTCGAGACAA 1421  
|||||  
DB 362 GGGCAGCTGTGTCACCATCTCGAGATCTAGACTCTGTGAGGTGTTCGAGACAA 303

QY 1422 GGTCTGGGATATTTGTGGAACCGACAGCACTCCAAAGGACTCCAGACCAATGTCT 1481  
|||||  
DB 302 GGTCTGGGATATTTGTGGAACCGACAGCACTCCAAAGGACTCCAGACCAATGTCT 243

QY 1482 TCAGGAAGGGCTGGGAGGCGATGAACCAAGTTCGCCACCTCAGCTGGGGCGGAGACC 1541  
|||||  
DB 242 TCAGGAAGGGCTGGGAGGCGATGAACCAAGTTCGCCACCTCAGCTGGGGCGGAGACC 183

QY 1542 TCCACACCCCTCCCTGTGGCGTCAACAAGACTCTCCGCCCTCCACGCACTGTACTCT 1601  
|||||  
DB 182 TCCACACCCCTCCCTGTGGCGTCAACAAGACTCTCCGCCCTCCACGCACTGTACTCT 123

QY 1602 TGTCAACAAGCTTAACCTGCTGTGTCTGTGGAGGCGCGCTGACATCTGGAC 1661  
|||||  
DB 122 TGTCAACAAGCTTAACCTGCTGTGTCTGTGGAGGCGCGCTGACATCTGGAC 63

QY 1662 ATGCTTAGCTGACGTAAGCTTTCCGCTTTCACCCCAATAAAGTCTTAATGCATCAAA 1721  
|||||  
DB 62 ATGCTTAGCTGACGTAAGCTTTCCGCTTTCACCCCAATAAAGTCTTAATGCATCAAGC 3

QY 1722 AA 1723  
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DB 2 AA 1

RESULT 8  
AA449322/c 429 bp mRNA linear EST 04-JUN-1997  
LOCUS AA449322

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
2x06e07.s1 Scores total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785700_3, similar to TR:G1280441 G1280441 DEGENERIN CHANNEL MDG. ;, mRNA sequence.	AA449322	AA449322	EST.	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	1 (bases 1 to 429)	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Giesel,G., Jost,S., Kuabab,T., Lacey,K., Le,N., Lennon,G., Merri,M., Martin,J., Moore,B., Schabelenberg,K., Steptoe,M., Tan,F., Theisling,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.	Washington University School of Medicine Contact: Wilson RK Unpublished (1997)	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone, similarity on wrong strand Seq primer: -41m3 fwd. ET from Amersham High quality sequence stop: 283. Location/Qualifiers
FEATURES	source	1..429								
		/organism="Homo sapiens"								
		/db_xref="GDB:5983318"								
		/db_xref="taxon:9606"								
		/clone_11b="IMAGE:785700"								
		/clone_11b="Scores_total_fetus_Nb2HF8_9w"								
		/dev_stage="8-9 weeks"								
		/lab_host="DH10B"								
		/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer (5' TGGTACCAATCTGAAGGGAGGCGCGCTTAATTTTTTTTTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Scores and M. Fatima Bonaldo. "								
BASE COUNT	89 a	100 c	151 g	89 t						
ORIGIN										
Query Match	23.2%	Score 401;	DB 9;	Length 429;						
Best Local Similarity	97.4%	Pred. No. 6e-66;								
Matches 418;	Conservative 0;	Mismatches 10;	Indels 1;	Gaps 1;						
1294	CAGAGAGGCGCTATGACATCTCAGACGCTGCTGGTGCATTTGGGGCCAGATGGGCGCTT	1353								
429	CGGAGAGGCGGTATGAATGTCAAGCGCTGTTGTGACATTTGGGGCCAGATGGGCGCTT	370								
1354	TTTCATCGGGGGCCAGCGCTGCT-CACCATCTCGAGATCTCAGACTACTCTGTGAGGTGTT	1412								
359	TCGAGCGGGGCCAGCGCTCTCTGACCATCTCTCGAGATCTCTAGACTACTCTGTGAGGTGTT	310								
1413	CCGAGACAAGGTCTCTGGGATATTTCTGGAAACGACAGCACTCTCCAAAGGACATCCAGC	1472								
309	CCGAGACAAGGTCCTGGGATATTTCTGGAAACGACAGCACTCTCCAAAGGACATCCAGC	250								
1473	CAATTCGCTTCAAGAGAGGCTGGGCGACGCCATCGAACCAGTTCCCGACCTTAGCTGGG	1532								
249	CAATTCGCTTCAAGAGAGGCTGGGCGACCATCGAACCAGTTCCCGACCTTAGCTGGG	190								
1533	CCCCGAGACTCCGACCCCTGCGCTGTGGCGGTACCAAGACTCTCTCCGCTCCACCGGAC	1592								
189	CCCCGAGACTCCGACCCCTGCGCTGTGGCGGTACCAAGACTCTCTCCGCTCCACCGGAC	130								

QY	1593	CHGCACCTGTGCACACAGCTCTACACCGTCGTGTGCTCTCGAGCCGCCCTGAC	1652
Db	129	CTGGTACCTGTGCACACAGCTCTACACCGTCGTGTGCTCTCGAGCCGCCCTGAC	70
QY	1653	ATTCGTGACATGCCCTGACAGCTGTTCCTTCCTTCACCCCAATAAAGTCCTAA	1712
Db	69	ATTCGTGACATGCCCTGACAGCTGTTCCTTCCTTCACCCCAATAAAGTCCTAA	10
QY	1713	TGCATCAAA 1721	
Db	9	TGCATCAAA 1	
RESULT 9			
LOCUS	AI684829	469 bp	linear
DEFINITION	wa6b06.x1 Soares_NFL_T_GBC_SI Homo sapiens cDNA clone		EST 07-MAR-2000
ACCESSION	IMAGE:2303027 3'	similar to TF:075906 075906	PROTON-GATED CATION
VERSION	CHANNEL SUBUNIT. ;		mRNA sequence.
KEYWORDS	AI684829		
ORGANISM	AI684829.1	GI:4896123	
REFERENCE	EST.		
AUTHORS	human.		
TITLE	Homo sapiens		
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
FEATURES	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
SOURCE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaps-rfemail.nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (infoimage.llnl.gov) for further information.		
	Insert Length: 563 Std Error: 0.00		
	Seq primer: -40UP from Gdbco		
	High quality sequence stop: 433.		
	Location/Qualifiers		
	1. 469		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2303027"		
	/clone_lib="Soares_NFL_T_GBC_SI"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with		
	a modified polylinker; Site.1: Not I; Site.2: Eco RI;		
	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NDHL19W, testis NH7, and B-cell		
	NCI-GCAP-GCBI) were mixed, and ss circles were made in		
	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The diver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I.M.A.G.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo.		
	BASE COUNT	101 a	107 c 151 g 110 t
ORIGIN			
	Query Match	22.3%	Score 386.8; DB 9; Length 469;
	Best Local Similarity	87.5%;	Pred. No. 2.9e-63;
	Matches 460; Conservative	0; Mismatches	7; Indels 59; Gaps 1;
QY	1207	AAGCTCAACCCGAGGAGGCTACTATCCCGGAGAACGTCGTGCGCCCTGACATCTTCTT	1266
Db	469	AAGCTCAACCCGAGGAGGCTACTATCCCGGAGAACGTCGTGCGCCCTGACATCTTCTT	410
QY	1267	GAGGCGCTCACTATGAGACCGTGAGAGAGAAGAAGCGCTATGAGATGTCAGAGCTGCTT	1326
Db	409	GAGGCGCTCACTATGAGACCGTGAGAGAGAAGAAGCGCTATGAGATGTCAGAGCTGCTT	350

QY	1337	GGTGACATTTGGGGGGGCACATGGGCTTTTCAATTCGGGGGACACCTGCATACCATCTTCGAG	1386
Db	349	GGTGACATTTGGGGGGGCACATGGGCTTTTCAATTCGGGGGACACCTGCATACCATCTTCGAG	290
QY	1387	ATCTAGACTACCTCTGTGAGGTGTTCGAGACAAGTCTTGGAATATTTCTGSAACGA	1446
Db	289	ATCTAGACTACCTCTGTGAGGTGTTCGAGACAAGTCTTGGAATATTTCTGSAACGA	230
QY	1447	CAGCACTCCCAAAGGACACTCCAGCACCATCTGCTTCAGGAAGGGCTGGGACCATCGA	1506
Db	229	CAGCACTCCCAAAGGACACTCCAGCACCAATTT-----	198
QY	1507	ACCCAAGTTCCCCAACCTGAGCGTGGGGCCCGACAGCTCCACCCCTCCCTGTGGCSTCAC	1566
Db	197	-----GACCTCCACCCCTCCCTGTGGCGCTCAC	169
QY	1567	AAGACTCTCCGCGCTCCACGACGACCTGTACCTTGTACACAGCTTAAACCTGCATG	1626
Db	168	AAGACTCTTTCGGCTCTCCCGCCGACACTGTACCTTGTACACAGCTTAAACCTGCATG	109
QY	1627	CTGTGTCTCTGGAGCCCGCCCTGACATCTGGAGCATGCGTACGCTGCAGCTAGCTTTTC	1686
Db	108	TTGTGTCTCTGGAGCCCGCCCTGACATCTGGAGCATGCGTACGCTGCAGCTAGCTTTTC	49
QY	1687	CGTCTCACCCCAATAAATGCTTAATGATCACAAAAAAAAAAAAAA	1732
Db	48	CGTTTTACCCCAATAAATGCTTAATGATCACAAAAAAAAAAAAAA	3

RESULT 10	LOCUS	AM742291	579 bp	mrna	linear	EST 07-SEP-2000
DEFINITION		u055b10.y1 Soares mouse NIE Mus musculus cdna clone IMAGE:2779963				
		5' similar to TR:035240 035240 PROTON GATED CATION CHANNEL DRASIC.				
		3' mRNA sequence.				

ACCESSION	AM742291	GI:7654076
VERSION	AM742291.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

**REFERENCE**  
**AUTHORS**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 579)  
 NCBI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE	JOURNAL	COMMENT
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
Tumor Gene Index		
Unpublished (1997)		
Other_ESTs: up55b10.x1		
Contact: Doherty, Steve, Ph.D.		

This clone is available royalty-free through LNL ; contact the IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Seq primer: -40RP from GIBCO  
High quality sequence stop: 480.

FEATURES	Location/Qualifiers
source	1. .579

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/organism="Mus musculus"
/strain="C3H x 101 (F1 stock)"
/db_xref="taxon:10090"
/clone_image="2779963"
/clone_id="Soares_mouse_NMIE"
/sex="male"
/dev_stage="newborn"
/lab_host="DH10B"
/note="Organ: inner ear, 170 pooled. Vector: pT73D-Pac;
Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed
with a Not I- oligo(dT) primer 15'
TGTACCAATCTGAAGTGGAGCGCGCCGACACTTTTTTTTTTTTTTTTTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized, and was constructed and donated by Bento
Soares and M. Fatima Bonaldo (University of Iowa) and R.

```

BASE COUNT	118 a	184 c	158 g	119 t
ORIGIN	Hardisty, A. Varela-Carver, P. Mburu and S.D.M. Brown (MRC UK Mouse Genome Centre and Mammalian Genetics Unit, Harwell, UK). <sup>a</sup>			

Query Match	20.6%	Score 357;	DB 9;	Length 579;
Best Local Similarity	81.0%;	Pred. No. 1.2e-57;		
Matches 430;	Conservative	0;	Mismatches 95;	Indels 6;
				Gaps 1;

706 GAGAGACCCCGTTTGGGTGGGATCCGAGTGCAGATCCACACGCCAGGAGGAGCGGCC 765

Db 55 GAAGAGACCCCATTTGAGGTGGGGATCCGAGTGCAGATCCACGGCCAGAGAGAACCCCT 114

766 ATCATCGATCAGCTGGGCTTGGGGGTGTCCCGGGCATCCAGACCTTTGTTCCTTGCCAG 825

115 GCGATTGACCAAGCTGGCTTCGCTGCTTGGCCCCAGGCCCCACGAGACTTTTGTCTCTCTGCGCAG 174

[illegible][illegible]

D5 1/5 CACAGCAGCTGAGTTTCTGCGACACACCCCTGGGGTGACTGCAGTACCGCATCTGTGGAT 234

886 CCCACTATGAGCCAGGCCCTCTGATCCCTAGGCTCCCCAGCCCCAGGCCCT 945

Db 235 CCCGACTTGTATCCAGAGCCCTCTGATCCCTGGGTTc-----CCCTAGCTCCAGCCCT 288

QY 946 CCCCATACCCCTTATG666GTGTGCGCCGTGGCTGCGAAAACCCGCTACGTTGGCTCGGAACTGC 1005

Db 289 CCTTATAGCTTAATFAGGGTGTGCGCTGGCCTGTAGTACGCTATGTGGCTCGGAAGTGC 348

QY 1006 GCGTCGCCGAATGGTGTACATGCCAGCGGACGTGCCAGTGTGCAGAGCCCGCCAGCAGTACAAG 1065

Db 349 GGATGTCGAATGATGCATATGCTGGAACCTCCCGAGTGTGCAGCCCCCAGCAGTACAAAG 408

1066 AACTGTGCCCAACCCGCCATAGATGCCATCCTTGCAGAGACTCTGGGCTGCCCAAC 1125

Db 409 GACTGTGCCAGCCCACTTGGACCTATGCTGCCAAGGACACTTGTCTGTCCAC 468

1126 CCGTCGCGCCAGCAGCGGCTTAGCCCAAGAGCTCTTCATGTGCGGATCCCGAGCCCGGCC 1185

469 CCGGCGCCCACTACACGGTATGCGCAAGGAGCTCCATGGTAGGAAATCCACAGCGGCGT 528

[illegible][illegible]

DB 529 TCAGCTCGCTACCTGGCCCGGAATACACCGTAGCGAGACTTACATCAG 5/9

## RESULT 1.1

A1179632/c	
A1179632	564 bp
LOCUS	MRNA
	linear
	EST 08-JAN-1999

**DEFINITION** ESR223356 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone RSPC181 3' end, mRNA sequence.

ACCESSION	AL179632	CT: A135170
VERSION	AL179632.1	

VERSION	01.4100175
ALL/5002.1	
KEYWORDS	
EST.	
NUMBER	

SOURCE	ORGANISM
Rattus sp.	Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 564)

**AUTHORS** Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.

JOURNAL  
of the  
Society for  
the Study of  
Social Problems  
45(1) 1-10  
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Sage Publications  
10.1177/0049124103251111  
http://jss.sagepub.com  
DOI: 10.1177/0049124103251111

COMMENT:  
On Oct 6, 1996 this sequence version replaced g1:3/302/0.  
Contact: Lee, NH

The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529  
Fax: (301)-838-0208

Email: [nhlee@tigr.org](mailto:nhlee@tigr.org)





REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia, Eutheria, Primates, Catarrhini; Homnidae; Homo.  
1 (pages 1 to 1059)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC).  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
source	1. .1059

BASE COUNT	270 a	285 c	319 g	183 t	2 others
------------	-------	-------	-------	-------	----------

## ORIGIN

Query Match	19.48;	Score 335.2;	DB 10;	Length 1059;
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Matches 540; Conservative 0; Mismatches 234; Indels 45; Gaps 2,

QY	612	GCTGCTCAACCACTACTAGGGGGGCGCATGGGCATAGGGGCGAGCATCATCTGGACCTGGA	671
Db	2	GGCGCTGAAAGACATAGGAAGGTGGGACCGGGCAATGGCGTGGAAATCATCTGGACATCCA	61
QY	672	GCAGAGGAGAAATATCTACTGTGTGTGGAGGAGACAATAGAGAGACCCCGTTTGTAGGTGGGGAT	731
Db	62	GCAGAGCAGATACCTGCTGTGTGGGGGAGACTACGAGAGCGTCCCTTGGAAAGCAGGCAT	121
QY	732	CCGAGTGCAGATCCACAGCCAGGAGGAGGCCCCCATCATCATCACTTGGGCTTGGGGGT	791
Db	122	CAAAATGACAGATCCCTAAGTACAGATGAACCTCTTCAATCGACACAGCTGGGCTTTGGCGT	181
QY	792	GTGCCCGGGGCAACAGACCTTTGTTCTTTGGCAGAGACGAGCTGAGCTTCCCTGGCAC	851
Db	182	GGCCCCAGGCTTCCAGACCTTTGTGGCCTGCGCAGAGACGCGGCTCATCTACTGGCCCC	241
QY	852	GCCCCGGGGCGATTGACATTCTCTGTGAACCCCACTATGAGCCAGAGCCCTCTGA	911
Db	242	AACCTGGGGGACCTGCAAAGCTGTATTACATGGAAGCTGGATTGGA-----	286
QY	912	TCCCTTAGGCTCCCCAGCCCGCCAGCCCTCCCTATACCTTATGGGTGTCCT	971
Db	287	-----TTTCTTCACTCTCTACACATCACGCTGCGGCAT	322
QY	972	GACCTGGCAAAACCGCTACGTGGCTCGGAGAGTGGCGGCTCCGAATGGTATACATGGCAG	1031
Db	323	CGACTGTAGAGAGCCCTACTGTGTGGAGACTGCAACTCCCGCATGTGTGCACACTGGCAG	382
QY	1032	CGAGCTGCCAGTGTGCAGCCCGCCAGCAGTACAAAGTAATGTGCCACCCGCGCATAGATGC	1091
Db	383	GGATCCCCCATCTACTCTCCAGAGACAGTACAAAGAGATGTGCAGATCCCTGTGGACTT	442
QY	1092	CATCTTGGCAAGAC-----TGGTGGCGTGGCCCCAACCCGCTGGCCAGCAGCGGCTA	1145

Db	443	CCTGGTGGAGAAGGCCGAGGATACCTGGGTGTGTAAATGCTTGCAACCTGACCCGGCTA	502
QY	1146	CGCCAAAGAGCTCTCCATATGTGTGGATATCCGAGCCGCGCGCGCGGCTCTCTGTGGCCG	1205
Db	503	TGGCAAAAGAGCTGTCCATATGTGTACATCCGACAAACCTCTGACCAAGTACTGTGGCAA	562
QY	1206	GAACTCAACCGCGACGAGGCGCTACATTCGCGGAGAACCTGTGTGGCCCTGGACATCTTCT	1265
Db	563	GAACTTCAACAAATCTGAGCAATACATATGGGGAGAACATCTGGTGGCTGGACATTTTCTT	622
QY	1266	TGAGGCCCTCAATATATGAGACCTGTGAGCAGAAAGACCTATGATGTAGAGACCTCT	1325
Db	623	TGAAGTCTCTCAACTATGTAGACCATTTGAACAGAGAAGGNCATATGATGTGCAAGGCTCTCT	682
QY	1326	TGGTGACATTTGGGGGCCAGATAGGGCTTTTATCTCGGGGCCACAGCTCATCATTCTCGA	1385
Db	683	GGGTATCATTCGGGGGCCAAAGATGGGGCTGTATCTCGGGGCCACAGCTCATCAGGTCTGGA	742
QY	1386	GATCCTAGACTACCTCTGTGAGGTCTTCCGAGCAAGGT	1424
Db	743	GCTCTTGTAGTACGCTTACGAGGCGATTATAGCACAAGCT	781

RESULT 14					
AI024055/c					
LOCUS	AI024055	503 bp	mRNA	linear	EST 27-AUG-1998
DEFINITION	ov72c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1642848				

ACCESSION	AI024055
VERSION	AI024055.1
KEYWORDS	EST.
SOURCE	human.

**REFERENCE**  
 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 503)  
**AUTHORS**  
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE**  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
**JOURNAL**  
 Unpublished (1997)  
**COMMENT**  
 Contact: Robert Strausberg, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: MCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/URL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 1003 Std. Error: 0.00  
Seq primer: -40m3 fwd. Err from Amersham  
High quality sequence stop: 137.

**SOURCE**

BASE COUNT	101 a	135 c	157 g	110 t
ORIGIN				

Query Match 18.9%; Score 326.8; DB 9; Length 503;  
 Best Local Similarity 84.6%; Pred. No. 66-52;  
 Matches 411; Conservative 0; Mismatches 2; Indels 73; Gaps 1;

QY 1236 GGAGAACGTGCTGGCCCTGGACATCTTCTTTGAGGCCCTCAACTATGAGACCGTGAGCA 1295  
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 DB 413 GGAGAACGTGCTGGCCCTGGACATCTTCTTTGAGGCCCTCAACTATGAGACCGTGAGCA 354  
 |||||||  
 QY 1296 GAAGAACGCTATGAGATCTGAGAGTGTGTGATGAGTGGGGCCAGATGGCCCTTTT 1355  
 |||||||  
 DB 353 GAAGAACGCTATGAGATCTGAGAGTGTGTGATGAGTGGGGCCAGATGGGGCTGTT 294  
 |||||||  
 QY 1356 CATCGGGGGCAGCTGCTGCTACCATCTCGAGATCTGAGACTCTGAGAGTGTTCG 1415  
 DB 293 CATCGGGGGCAGCTGCTGCTACCATCTCGAGATCTGAGACTCTGAGAGTGTTCG 234  
 |||||||  
 QY 1416 AGACAAAGTCTCGGATATTTTGGAAACGAGACAGCACTCCCAAGGCACTCCAGACCAA 1475  
 |||||||  
 DB 233 AGACAAAGTCTCGGATATTTTGGAAACGAGACAGCACTCCCAAGGCACTCCAGACCAA 174  
 |||||||  
 QY 1476 TCTGCTGAGAAAGGCTGGGAGCCATGGAACCAAGTTCCCACTGAGCTGGGCC 1535  
 |||||||  
 DB 173 TCTGCTGAGAAAGGCTGGGAGCCATGGAACCAAGTTCCCACTGAGCTGGGCC 114  
 |||||||  
 QY 1536 CAGACCTCCACCCCTCCCTGTGCCGTACCAAGACTCTCCGCCCTCCACCGACCTG 1595  
 DB 113 ----- 114  
 |||||||  
 QY 1596 CTACCTGTGACACAGCTCTAGACCTGCTGTGTGCTCGAGACCCCGCCCTGACATC 1655  
 |||||||  
 DB 113 ----- 67  
 |||||||  
 QY 1656 CTGACATGCTAGCTGAGCTAGCTTTTCCGTCTACCCCAATAAAGCTCAATGC 1715  
 |||||||  
 DB 66 CTGACATGCTAGCTGAGCTGAGCTTTTCCGTCTACCCCAATAAAGCTCAATGC 7  
 |||||||  
 QY 1716 ATCAAA 1721  
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 DB 6 ATCAAA 1

RESULT 15  
 B1548575 835 bp mRNA linear EST 05-SEP-2001  
 LOCUS 603189513F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5260899 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1548575  
 VERSION B1548575.1 GI:15435887  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 835)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bbs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shireki  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1AM1657 row: j column: 04  
 High quality sequence stop: 831.  
 Location/Qualifiers  
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 /lab\_host="DH10B"  
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 ); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
 size-selected for average insert size 2.5 kb and  
 normalized to ROT 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NIH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."  
 BASE COUNT 167 a 282 c 229 g 157 t  
 ORIGIN

Query Match 18.8%; Score 325.6; DB 10; Length 835;  
 Best Local Similarity 98.8%; Pred. No. 1e-51;  
 Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1150 AAGAGCTTCCATGCTGGGATCCCGAGCCGCCGCCGCTTCTGACCCGGAAG 1209  
 |||||||  
 DB 6 AAGAGCTTCCATGCTGGGATCCCGAGCCGCCGCCGCTTCTGACCCGGAAG 65  
 |||||||  
 QY 1210 CTCACCGCAGGAGGCTTCATCGCGGAGAGCTGTGCGCCCTGAGATCTTTTGAG 1269  
 |||||||  
 DB 66 CTCACCGCAGGAGGCTTCATCGCGGAGAGCTGTGCGCCCTGAGATCTTTTGAG 125  
 |||||||  
 QY 1270 GCCCTCAACTATGAGACCGTGAGAGCAAGAGCCATGAGATGTCAGAGCTGCTGGT 1329  
 |||||||  
 DB 126 GCCCTCAACTATGAGACCGTGAGAGCAAGAGCCATGAGATGTCAGAGCTGCTGGT 185  
 |||||||  
 QY 1330 GACATTTGGGGGCAATGGGCTTTTCATCGGGGCGACCTGCTACCATCTCGAGATC 1389  
 |||||||  
 DB 186 GACATTTGGGGGCAATGGGCTTTTCATCGGGGCGACCTGCTACCATCTCGAGATC 245  
 |||||||  
 QY 1390 CTAGACTACCTCTGAGAGTGTTCGAGACAAGTCTGAGATTTTGTGAAACGAGAC 1449  
 |||||||  
 DB 246 CTAGACTACCTCTGAGAGTGTTCGAGACAAGTCTGAGATTTTGTGAAACGAGAC 305  
 |||||||  
 QY 1450 CACTCCCAAGGCACTCCAGACCAATCTGCT 1481  
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 DB 306 CACTCCCAAGGCACTCCAGACCAATCTGCT 337  
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Search completed: October 11, 2002, 04:18:56  
 Job time : 1974 secs





Accession	Sequence	Position
Db	1345 GGAGCAAGCCGCTTACCATCCTTGAGATCCTGACTATCTGTGAGGTTTTCCAAAC	1404
Qy	1420 AAGTCTCGGATATTTCTGGAACCGACAGCACTCCCAAGAAGCACTCCAGCACCAATGTG	1479
Db	1405 AGATCTCTGGGGTATTTCTGGAACAGAAAGAGCGCTCAAAACGCTCTGGCAACACTGTG	1464
Qy	1480 CTTCAGGAAGGGCTGGGACACCAATCGAACCCAGTGTCCCACTAGCTGGGGCCCAAGA	1539
Db	1465 CTCAGGAAGAGTTGATATGGCCATCGAACACATGTTCCCACTAGCTTAGGGCCCAAG	1524
Qy	1540 CCTCCCAACCCCTCCCTGTCGCGTACCAAGACATCTCCGCTCCCAACGCAAGCTGTAC	1599
Db	1525 CCTCTTACCACTCCCTGTGCTGTACCAAGACACTCTTGCTCCCAACCGTACTGTTAC	1588
Qy	1600 CTTGTCACACAGCTGTAG	1617
Db	1585 CTCGTCAAGAGCTGTAG	1602

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RESULT 3
US-09-360-197-7
; Sequence 7, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Dweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989 6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3647
; TYPE: DNA
; ORGANISM: ratus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(1785)
US-09-360-197-7

Query Match          27.2%; Score 470.6; DB 4; Length 3647;
Best Local Similarity 58.9%; Pred. No.4e-102;
Matches 924; Conservative 0; Mismatches 579; Indels 66; Gaps 4;

OY      5  ACGAGCGGTTCTGCGCCATGAAGCCCACTCAGCGCCAGAGAGGCGCGGCGGACGCCCT 64
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      230 AAGAGGAAGAGAGAAATGAGGCGAGGCGAGTTGGATGAGGCGTGTGACTACCTA 289

OY      65  CGGAGATCCGCGTGTTGCCAGCACTCTCATGTCACGCGCGTGGGCCACGTTCGGGC 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      290 GGGACTGTGTGCGCTTCGCCAACACTGTACTTTCATGTGTCCAGCAGCATGTGTTGG 349

OY      125 CAGGACCGCTGAGCTGCGCCGCGGGGATGTGGGACAGCGCCGTGTCTGTACGTGGCCA 184
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      350 AAGGGGCGCCAGGCGCCAGGCGAGGCGCTTATGGGCAGTGGCCTTTGTCAATGACACTGGGT 409

OY      185 CCTTCTCTACAGGTGTGCTAGAGGATGCGCTACTACAGGAGTTCACACCACTGACTG 244
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      410 CCTTCTCTGTCCAGGTAGGGGACCCGCTGTATTATTACCTCAGCTACCAACACGTGACTT 469

OY      245 CCTGTGATGAGGAGAAAGCCACCGGGCTGCTTCCCGGCTGTCAACCGTGTCAACATCA 304
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      470 TGTATGAGAGAGATGCGCCACCGAGGAGCTGTGCTTCCCACTGTCTACCTTCTGTCAACACCA 529

```

```
QY 305 ACCCACTGCGCGCTGCGGCTTAAGCCCAAGCACTGCATGGGCTGCGCGCTGC 364
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Db 530 ATGCCCTGGGGTGTCCAGCTCAGCTACCTGACTTGGCTCT--ACCTGGCCCATCAG 586
QY 365 TGGGCTGAGTCCCGAGAGCAAGCGGCTTCCTGGCGCGCCCGGCGCCCGCTGCAC 424
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Db 587 TAGGACTGAGTGAAGTGAAGACCCCGGGGTGC-----CTTGGCTCTCTCG 634
QY 425 CGCGCGCTTCAATGACCACTCCACCTTTGACATGGCGCACTATGCGCGTGCAGG 484
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Db 635 GCCCAAGGCTTTCCTCGGGGAGGCTTTTAACCTCCATCCTTTCTAATGCGCTTGGC 654
QY 485 ACTCCCTGATGACATGCTGCTGGAGTGTGCTTCCGTGGCCAACTTGTGGGCTGAGA 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 ACCGCTGGAGGACATGCTGCTCTATTGTTCATGTTGGGGGCGCCCTGGTCCACACA 754
QY 545 ACTTCAACCAAGATCTTACCCCGATGGGAAAGTGTACACATTTAACTCTGGGCTGATG 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 ACTTCTCAATGCTTCTCACTCGGTATGGGAAGTGTACACATTCAACTCGGGCCAAAGATG 814
QY 605 GGGCAGAGCTGCTACACCACTACTAGGGGTGCGCATGGGCAATGGGCTGACATCATGCTGG 664
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Db 815 GCGGCGCAGGCGCTGAAGACCATGAAGAGTGGGACTGGCAATGGCTGGAGATATGCTGG 874
QY 665 ACGTGAGAGAGAGAAATATCTACTGTGTGAGAGCAATGAGAGACCCGTTTGAGG 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 875 ACATTCAGCAAGATGAATATTTGCTGTGTGGGAGAGACCGCAGACATCCTTGGAGG 924
QY 725 TGGGGATCCGAGTGCAGATCCACAGCAGAGAGAGCGCCCATCATGATCAGCTGGGCT 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 935 CAGGCAATCAAGTGCAGATCCACAGTCAAGTGAATGACCCCTTTCATCAGCCACTGGGCT 994
QY 785 TGGGGGTGTCGCCGGGCTACAGACCTTTGTTTCTTGCCAGCAGCAGCATGAGCTTGC 844
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Db 995 TTGGTGTGGCTCCAGGTTTCAGACCTTGTGTCTTGCCAGAGAGCAGAGGCTATATCTACC 1054
QY 845 TGCACACCGCTTGGGGCGATGTCAGTTGAGCATCTCTGAACCCCACTATGAGCCAGAGC 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1055 TGCCTTCACCTGGGGCAGCTGCAATGTGTACATGTGAGCTGGATTT----- 1103
QY 905 CCTGTGATCCCTAGGCTGCCCAAGCCCAAGCCCTCCCTATACCTTATGGGCT 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 -----CTTCAAGTCTCTACACATCACTGCGCT 1129
QY 965 GTGCGCTGCGCTGCGAAACCCGCTACGTGGCTCGGAAGTGGGCTGCCGAATGGTGACA 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1130 GCGGGAATTAATGCGAGAGCGCTTACTGTGTGAGAACTGCAACTCCGTATGTGTACACA 1189
QY 1025 TGCAGAGCAGCTGCGAGTGTGAGCCGCCAGCAGTACAAGAACTGTGCCACCGGCGCA 1084
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Db 1190 TGCAGAGGAGCGCCCATCTGACTGCAGAGAGTACAAGAGTGTGAGATCTGTGCC 1249
QY 1085 TAGATGCCATCTCT-----TGCAGAGACTCGTGGCGCTGCCCAACCGCTGGGCCAGCA 1138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1250 TGGACTTCTTAATGAGAAAGAACCAAGAAATACGCTGTGTGAGAGCTTGTGCAACTGA 1309
QY 1139 CGCGCTACCCAGAGAGCTCTCATGGTGGATCCGAGCCGCGCGCGCGCGCTTTC 1198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1310 CCGCGTAGGCGCAAGAGCTGTCTCATGTGTCAAGATCCCAAGCAAGAGCTCCGCCAATTACC 1369
QY 1199 TGGCCCGGAAGTCAACCGCAGCGAGGCTACATCGCGGAAGAACTGTGGCCCTGAGACA 1258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1370 TGGCGCAAGAAATCAACAATCGAGACAGTACATAGGGGAGAAACATTTGTGCTGAGACA 1429
QY 1259 TCTTCTTTAGGCGCTCAACTATGAGACCGTGGAGAGAAAGGCTTATGAGATGTGAG 1318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1430 TTTTCTTTTAAATCTCTCAACTATGAGACCATGAGCAAGAAAAGGCTTATGAGATGTGAG 1489
QY 1319 ACCTGCTTGTATGAGGAGCAGATGGGCTTTTCACTGGGAGGCGCAGCTGCTGACACA 1378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1490 GCGTGTGGGTGACATCGGGGCGCAGATGGGTTGTTCATCGGTGCCACATCTCTACCG 1549
QY 1379 TCCTCGAGATCTAGACTCTCTGTGTGAGGTGTTCGAGACAAGGTCCTGGGATATTTCT 1438
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Db 1550 TGTGTGAACCTTTTGAATATGCTACGAGTCAATTAAGCACAGGCTGTGCAGACGGGAA 1609
QY 1439 GGAACGAGACGACTCCCAAGGACACTCCAGACACCAATCGCTTTCAGGAAGGCGGGACA 1498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1610 AGTGCCAGAAAGAGGCTTAAGAGAGCAGCGACAGACAAAGGCGGTGCGCTCAGCTGTGATG 1669
QY 1499 GCCATGAAACCAAGTTCCCACTCAGCTTGCGGCCCGCCAGACCTCCACCCCTGCTGTG 1558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1670 ACGTCAAAAGACACAATCCCTGGAGAGGCTCCGAGAGACATCTCTGCGGGATGACGTAGG 1729
QY 1559 CCGTCAACA 1567
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Db 1730 CTGCGCAACA 1738
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RESULT 4
US-09-360-197-3
; Sequence 3, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldebrand, Rainer
; APPLICANT: Dewelle, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; FILE REFERENCE: 989,6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
US-09-360-197-3
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Query Match 26.4%; Score 456.8; DB 4; Length 1620;  
Best Local Similarity 58.5%; Pred. No. 5.5e-99;  
Matches 893; Conservative 0; Mismatches 567; Indels 66; Gaps 3;

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QY 69 CATCCGCTGTGTCGCCAGCAACTGCTCGATGCAAGCGGCTGGGCAAGTCTGGGCGCAGG 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9 CATCCAGGCGCTTGGCAGCAGCTCCACTGACAGCGGCAATGCGGCACATCTTCTCTACAGA 68
QY 129 CAGCTGAGCCTGCGCGCGGGGATGTGGGCAAGCGGCGCTGTCTGTCTGACAGTGGCACCTT 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 GCGGCTGTCTGTGAACGCGGCACTGTGGGCGCTGTCTGTGGGCTCTGCGGTGTGTGCT 128
QY 189 CCTCTACAGGTGGCTGAGAGGGTGGCTGACTACAGAGGATTCACACAGACAGTCCCT 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 GCTGTGTGTGTCAGGAGCGGTGTGCACTACTTCCACTACACACATGTCTACCAAGCT 188
QY 249 GGTATGAGAGAAAGCAGCAGGCTGTCTTCCGCGCTGTACACCTGTGCAATCAACCC 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 CGACGAGGTGGCTGCTCAGCTTCAAGCTTCCCTGTGTGTGTCAGAGTGTGCAACTCAAGA 248
QY 309 ACTGCGCGCTGCGCGCTTCAAGCCCAAGCACTGCACTGGGCTGGGCTGTGCGCTG----- 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 GTTCCGCTTTAGCAAGTCTCCAAAGATGACCTGTATCATGTGGGAGACTGCTGCGCCCT 308
QY 364 -----CTGGGCTGTGATCCGCAAGAGCAGCGCGGCTTCTGTGCGGCGCT 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 GCTCAACAACAGTATGAGATACAGACACACAGATGCGAGATGAAMAGCTGGAGAT 368
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OY 502 CTGCTGAGACTGCGCTTCCTGCGCCAACTGTGGGCTGAGAACTTCACACGATCTTC 561
    |||||  ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 627 CTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
OY 562 ACCCGGATGGGAAAGTGCATACATTTTAACTGCGCGTGAATGGGCGAGAGCTGCTCAC 621
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 687 ACTCGGATGGGAAAGTGCATACATTTTAACTGCGCGTGAATGGGCGAGAGCTGCTCAC 746
OY 622 ACTACTAGGGGTGGGCAATGGGCGTGCATATCATGCTGAGCTGAGCTGAGAGAGAA 681
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 747 ACCATGAAAGTGGGAGCTGAGTGGGCGTGGGAGTATCATGCTGAGCTTACAGAAATGAA 806
OY 682 TATCTACTGTGTGAGGAGCAATAGAGAGACCCGTTTGTAGTGGGAGTCCGATGCGAG 741
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 807 TATTTGCTGTGTGGGAGAGAGACCGAGCATCTCTTGAAGAGAGCATCAAGATGCGAG 866
OY 742 ATCCAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 801
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 867 ATCCAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926
OY 802 TACAGAGCTTTTCTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 927 TTCCAGAGCTTTGTGTCTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
OY 862 GATTGCACTTACAGATCTCTGAGAACCCCACTATGAGAGAGAGAGAGAGAGAGAGAG 921
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 987 ACTCTCAATGCTGTATACCATGAGATCTGAGATTT----- 1018
OY 922 TCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 981
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1019 -----CTTGCATCTCTACAGATCTGCTGCGGAGTTGATTTGCGAG 1061
OY 982 ACCCGCTACGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1041
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1062 ACCGCTTACGTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1121
OY 1042 GTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1097
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1122 TACTGCTACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1181
OY 1098 --TGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1155
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1182 AAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1241
OY 1156 CTCTCATGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1215
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1242 CTGTCTCATGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1301
OY 1216 CGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1275
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1302 AAATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1361
OY 1276 AACTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1335
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1362 AACTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1421
OY 1336 GGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1395
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1422 GGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1481
OY 1396 TACCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1455
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1482 TATGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1541
OY 1456 CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1515
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1542 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1601
OY 1516 CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1602 CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1653

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RESULT 6
US-09-360-197-5
; Sequence 5, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Basillana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Dewelle, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989.6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1666
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(1663)
US-09-360-197-5

Query Match      24.0%; Score 416.2; DB 4; Length 1666;
Best Local Similarity 58.6%; Pred. No. 2.1e-89;
Matches 842; Conservative 0; Mismatches 523; Indels 72; Gaps 4;

OY 20 CCATGAGCGCCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 126 CGATGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
OY 80 TCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 139
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 186 TTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
OY 140 TCGCGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 199
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 246 TCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 305
OY 200 TGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 306 GCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 365
OY 260 AAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 366 TGGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
OY 320 CGCGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 379
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 426 CGAGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
OY 380 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 486 ACGTCAAGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
OY 425 CGCCGCGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 546 AGGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
OY 479 CTGGGCACTCCCTGATATACATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 606 TGGGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
OY 539 CTGAGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 666 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 725

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QY 775 CAGTGGGCTGGGGTGTCCCGGCTACAGACCTTTGTTCTTGCCAGACGAG 834
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Db 943 GAGCTGGCTTGGGGTGGCTCCGGGTTCCAGACCTTGTGGCCACAGAGCGAGG 1002
QY 835 CTGAGCTTCTGCGACCGCTGGGGCGATTGCGATCTCTGAACCCCACTAT 894
    || || || || || || || || || || || || || || || || || || || || ||
Db 1003 CTGACATATCTGCCCCCAGCATGGGGGAGTGGCGGTCTCTCAGAGATGGAGCTGACT-- 1060
QY 895 GAGCCAGAGACCTCTGATCCCTAGGCTCCCGACGCCCAAGCCCTCCCTATACC 954
    || || || || || || || || || || || || || || || || || || || || ||
Db 1061 -----TCTTCTCTGTTTACAGC 1077
QY 955 CTTATGGGTTGCGCTGCGCTGCGAAGCCGCTAGCTGGTGGAGTGGCGGCTCCCA 1014
    || || || || || || || || || || || || || || || || || || || || ||
Db 1078 ATCAGAGCTGTGGATTGATGTGAGACCCGCTACATGTGAGATCTTAATCTCCCG 1137
QY 1015 ATGTGTATCATGCGAGCGCTGCGATGTGCGAGCCCGCAGCATGACAAAGATGTGCC 1074
    || || || || || || || || || || || || || || || || || || || || ||
Db 1138 ATGTGTACATGCGAGGAGCGCGCTTCTGACCCCTGAGAGAGCAGCAAGAGTGTGCA 1197
QY 1075 CACCGGCGCATGATGATGCTCTTGGCAAGAC-----TGTGCGCTGCCCCAACCG 1128
    || || || || || || || || || || || || || || || || || || || || ||
Db 1198 GAGCTGCGCTGCTGCTACTGCGAAGAAAGACAGCAATTAATGCTGTGCGAGACACCC 1257
QY 1129 TGGGCGAGAGCGGCTAGCGCAAGAGCTCTCCATGTGCGATGCCGAGCCGCGCGCC 1188
    || || || || || || || || || || || || || || || || || || || || ||
Db 1258 TCGAACCTGACAGCTACAAAGAGCTCTCCATGTGTAAGTCCCGCAGAGAGCTCA 1317
QY 1189 GCGCGCTTCTGCGCGGAGAGCTCAACCGCAGGAGGCTTACATGCGAGAACTGTCTG 1248
    || || || || || || || || || || || || || || || || || || || || ||
Db 1318 GCGAGTACTTGAAGAGAAATTTAGCAAAATGGAATAATATCTCAGAGAACTATCT 1377
QY 1249 GCCCTGAGCATCTTCTTGAAGGCTCAACTATGAGACCGTGAGAGAGAAAGGCTTAT 1308
    || || || || || || || || || || || || || || || || || || || || ||
Db 1378 GTTCTGAGCATATTTTGTAGGCGCTCAATGAGAAATGAAAGAGAGGCTAT 1437
QY 1309 GAGATGAGAGCTGCTGTGATGATGAGGGGCGAGATGGGCTTTCATCGGCGGCGAC 1368
    || || || || || || || || || || || || || || || || || || || || ||
Db 1438 GAGATGAGAGCTTACTTGTGATGATGAGGGGCGAGATGGGCTTTCATGCTGTAG 1497
QY 1369 CTGCTCACCATCTCGAGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1428
    || || || || || || || || || || || || || || || || || || || || ||
Db 1498 CTGCTCACCATCTCGAGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1557
QY 1429 G 1429
Db 1558 G 1558

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RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300,6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F1s
US-08-232-463-14

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Query Match 2.9%; Score 50.4; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred. No. 0.0086;
Matches 15; Conservative 210; Mismatches 151; Indels 0; Gaps 0;

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QY 1323 GCTTGTGATGATGGGGGCGAGATGGGCGCTTTTCATCGGGGCGCGCTGCTACATCGT 1382
    ||||||| || || || || || || || || || || || || || || || || || || || || || ||
Db 1037 GCTTGTGATGATGGGGGCGAGATGGGCGCTTTTCATCGGGGCGCGCTGCTACATCGT 1096
QY 1383 CGAGATCTAGATCTGCTGTGAGTGTCCGAGACAGATGCTGGATATTTCTGGA 1442
    || || || || || || || || || || || || || || || || || || || || ||
Db 1097 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1156
QY 1443 CCGACAGCACTCCCAAGGCACTCCAGCACCAATCTGCTTACAGAGGCGTGGCGACCA 1502
    || || || || || || || || || || || || || || || || || || || || ||
Db 1157 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1216
QY 1503 TCGAACCAAGTCCCGCCTGAGCTGAGGCGGCGCGACGCGCCGCGCTGCGCGG 1562
    || || || || || || || || || || || || || || || || || || || || ||
Db 1217 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1276
QY 1563 CACCAAGACTCTCCGCTCCGCGACGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1622
    || || || || || || || || || || || || || || || || || || || || ||
Db 1277 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1336
QY 1623 CTGCTGTGCTGCTGCGAGCGCGCGCTGACATCTGAGATGCTGAGATGCTGAGCT 1682
    || || || || || || || || || || || || || || || || || || || || ||
Db 1337 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1396
QY 1683 TTTCCGCTTCACCC 1698
Db 1397 YYYYYYYYYYYYYY 1412

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RESULT 10
US-08-997-080-133
; Sequence 133, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA

```

```

: COUNTRY: USA
: ZIP: 98121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,080
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sleath, Janet
: REGISTRATION NUMBER: 37,007
: REFERENCE/DOCKET NUMBER: 11000.1007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-269-0565
: TELEFAX: 206-269-0563
: TELEX:
: INFORMATION FOR SEQ ID NO: 133:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 742 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
US-08-997-080-133

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Query Match      2.5%; Score 43.8; DB 2; Length 742;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

OY 1088 ATGCATCTTCGCGAAGACTGTCGCGCTCCCAACCCGTGGCCACGAGCGGCTACG 1147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 AGGGGATCGCTTGCAGACACGCGCGCGAGCGCGCTGTGCGCCGCAATGCCAGAT 427

OY 1148 CCAAGAGACTCTCCATGATGTCGGATCCGAGCGCGCGCGCGCTTCCGTGGCCGGA 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 TCAACGAGTTTTCGCCGAGATCGTGACACCGCTTCACTTGAGAGATGTGATGCTGCG 487

OY 1208 AGCTCAACCGCAGGAGCGCTACATCGCGGAGAACGTGCTGGCCCTGACATCTTCTTTG 1267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 ACCTCAGAGGACAGGTGTGATCGCGCTACCAAGGGGCGGATCTCGGCAACAATCG 547

OY 1268 AGGCCCTCACTATGAGACCGCTGAGCAGAAAGAGCCCTATGAGATGTGAG 1318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 TCAACGGCCCTATCGCAACCGGAGAACTGTGGAAGCCTACGAGAAAGCGG 598

```

```

RESULT 11
US-08-997-362-133
: Sequence 133, Application US/08997362
: Patent No. 5985287
: GENERAL INFORMATION:
: APPLICANT: Tan, Paul
: APPLICANT: Hiyama, Jun
: APPLICANT: Visser, Elizabeth
: APPLICANT: Skinner, Margot
: APPLICANT: Prestidge, Ross
: TITLE OF INVENTION: TREATMENT AND METHODS FOR MYCOBACTERIAL INFECTIONS
: NUMBER OF SEQUENCES: 194
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Law Offices of Ann W. Speckman
: STREET: 2601 Elliott Avenue, Suite 4185
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98121

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,362
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
: FILING DATE: June 12, 1997
: APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
: FILING DATE: August 29, 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sleath, Janet
: REGISTRATION NUMBER: 37,007
: REFERENCE/DOCKET NUMBER: 11000.1002c2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-269-0565
: TELEFAX: 206-269-0563
: TELEX:
: INFORMATION FOR SEQ ID NO: 133:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 742 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
US-08-997-362-133

```

```

Query Match      2.5%; Score 43.8; DB 2; Length 742;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

OY 1088 ATGCATCTTCGCGAAGACTGTCGCGCTCCCAACCCGTGGCCACGAGCGGCTACG 1147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 AGGGGATCGCTTGCAGACACGCGCGCGAGCGCGCTGTGCGCCGCAATGCCAGAT 427

OY 1148 CCAAGAGACTCTCCATGATGTCGGATCCGAGCGCGCGCGCGCTTCCGTGGCCGGA 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 TCAACGAGTTTTCGCCGAGATCGTGACACCGCTTCACTTGAGAGATGTGATGCTGCG 487

OY 1208 AGCTCAACCGCAGGAGCGCTACATCGCGGAGAACGTGCTGGCCCTGACATCTTCTTTG 1267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 ACCTCAGAGGACAGGTGTGATCGCGCTACCAAGGGGCGGATCTCGGCAACAATCG 547

OY 1268 AGGCCCTCACTATGAGACCGCTGAGCAGAAAGAGCCCTATGAGATGTGAG 1318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 TCAACGGCCCTATCGCAACCGGAGAACTGTGGAAGCCTACGAGAAAGCGG 598

```

```

RESULT 12
US-09-095-855-133
: Sequence 133, Application US/09095855
: Patent No. 6160093
: GENERAL INFORMATION:
: APPLICANT: Tan, Paul
: APPLICANT: Visser, Elizabeth
: APPLICANT: Skinner, Margot
: APPLICANT: Prestidge, Ross
: TITLE OF INVENTION: Compounds and Methods for Treatment and Diagnosis of Mycobacterial Infections
: NUMBER OF SEQUENCES: 208
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Law Offices of Ann W. Speckman
: STREET: 2601 Elliott Avenue, Suite 4185
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,855  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/705,347  
FILING DATE: 29-AUG-1996  
APPLICATION NUMBER: 08/873,970  
FILING DATE: 12-JUN-1997  
APPLICATION NUMBER: 08/997,362  
FILING DATE: 23-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sleath, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000.1002c3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 742 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-095-855-133

Query Match 2.5%; Score 43.8; DB 4; Length 742;  
Best Local Similarity 49.4%; Pred. No. 0.15;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1088 ATGCATCTTCCGCAAGAGACTGTGGCCGCCCAACCGCTGCGCCAGCAGCAGCGCTACG 1147  
DB 368 AGCGGATCGCGTTGCGAGACGCGCGCGGCGGCGCGCTGTGGCGCCATGCGAGAT 427  
QY 1148 CCAAGAGCTCTCCATGATGCGGATCCGACCGCGCGCGCTTCTGCGCCGGA 1207  
DB 428 TCACGAGCTTCTCCGCGAGATCGTCACCGCTTCAACTTCGAGATCTGCTCTCG 487  
QY 1208 AGCTCAACGCGGAGCGCTACATCGCGGAGAGAGCGCTGCGCGGAGCATTTCTTG 1267  
DB 488 ACCTCGAGGCGACGCTGTGCTACTCCGCTACAGGCGCGGATCTCGGACCAACATCG 547  
QY 1268 AGCCCTCACTATGAGACCGTGGAGCAGAGAAGGCTATGAGATGTGAG 1318  
DB 548 TCACGCGCCCTATCGCAACCGGGAAGTGTGGAAGCTATGAGAGAGCGCG 598

RESULT 13  
US-09-324-542-133

Sequence 133, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

TITLE OF INVENTION: Methods and Compounds for the Treatment

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 133

LENGTH: 742

TYPE: DNA

ORGANISM: Mycobacterium vaccae

US-09-324-542-133

Query Match 2.5%; Score 43.8; DB 4; Length 742;  
Best Local Similarity 49.4%; Pred. No. 0.15;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1088 ATGCATCTTCCGCAAGAGACTGTGGCCGCCCAACCGCTGCGCCAGCAGCAGCGCTACG 1147  
DB 368 AGCGGATCGCGTTGCGAGACGCGCGCGGCGGCGCGCTGTGGCGCCATGCGAGAT 427  
QY 1148 CCAAGAGCTCTCCATGATGCGGATCCGACCGCGCGCGCTTCTGCGCCGGA 1207  
DB 428 TCACGAGCTTCTCCGCGAGATCGTGCAACGCTTCAACTTCGAGATCTGCTCTCG 487  
QY 1208 AGCTCAACGCGGAGCGCTACATCGCGGAGAGAGCTGTGCGCTTCTGCGCATTTCTTG 1267  
DB 488 ACCTCGAGGCGACGCTGTGCTACTCCGCTACAGGCGCGGATCTCGGACCAACATCG 547  
QY 1268 AGCCCTCACTATGAGACCGTGGAGCAGAGAAGGCTATGAGATGTGAG 1318  
DB 548 TCACGCGCCCTATCGCAACCGGGAAGTGTGGAAGCTATGAGAGAGCGCG 598

RESULT 14

US-08-997-080-122

Sequence 122, Application US/08997080

Patent No. 5968524

GENERAL INFORMATION:

APPLICANT: WATSON, JAMES D.

APPLICANT: TAN, PAUL L.J.

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-

CORRESPONDENCE ADDRESSES: 194

ADDRESS: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,080

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 122:

SEQUENCE CHARACTERISTICS:

LENGTH: 898 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-08-997-080-122

Query Match 2.5%; Score 43.8; DB 2; Length 898;  
Best Local Similarity 49.4%; Pred. No. 0.15;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1088 ATGCATCTTCCGCAAGAGACTGTGGCCGCCCAACCGCTGCGCGAGCAGCAGCGCTACG 1147

Db 524 AGGCGATGCGCTTCGACGACGCGCGCGCGCGCGCTGCTGCGCGCCCAATGCCAGAT 583  
OY 1148 CCAAGAGCTCTCCATGATGGGCGATCCGAGCGCGCGCGCGCGCTTCCGCGCGCGGA 1207  
Db 584 TCAACGAGTCTTCCCGCGAGATGTCACCGCTTCAACTTCAGAGATCTGATGCTGCG 643  
OY 1208 AGCTCAACCGCAGCGAGCGCTTACATCGCGGAGAACGCTGCGCGCTTGACATCTTCTTG 1267  
Db 644 ACCTGAGGCGCAACGTGGTGTACTCCGCTACAAAGGGCGCGGATCTCGGGACAAACATCG 703  
OY 1268 AGCCCTCAACTATGAGACCGTGGAGCAGAGAACGCGCTATGAGATGTCAG 1318  
Db 704 TCAACGCGCCCTATCGCAACCGGGAATCTGCGAAGCCTTACGAGAAAGCGG 754

RESULT 15  
US-08-997-362-122

; Sequence 122, Application US/08997362  
; Patent No. 5985287  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Hiyma, Jun  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Scott, Linda  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR  
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,362  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970  
; FILING DATE: June 12, 1997  
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347  
; FILING DATE: August 29, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleeth, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1002c2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 898 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; US-08-997-362-122

## Query Match

2.5%; Score 43.8; DB 2; Length 898;

Best local similarity 49.4%; Pred. No. 0.15; Mismatches 117; Indels 0; Gaps 0;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Search completed: October 11, 2002, 04:20:32  
Job time : 109 secs

Db 524 AGGCGATGCGCTTCGACGACGCGCGCGCGCGCGCTGCTGCGCGCCCAATGCCAGAT 583  
OY 1148 CCAAGAGCTCTCCATGATGGGCGATCCGAGCGCGCGCGCGCGCTTCCGCGCGCGGA 1207  
Db 584 TCAACGAGTCTTCCCGCGAGATGTCACCGCTTCAACTTCAGAGATCTGATGCTGCG 643  
OY 1208 AGCTCAACCGCAGCGAGCGCTTACATCGCGGAGAACGCTGCGCGCTTGACATCTTCTTG 1267  
Db 644 ACCTGAGGCGCAACGTGGTGTACTCCGCTACAAAGGGCGCGGATCTCGGGACAAACATCG 703  
OY 1268 AGCCCTCAACTATGAGACCGTGGAGCAGAGAACGCGCTATGAGATGTCAG 1318  
Db 704 TCAACGCGCCCTATCGCAACCGGGAATCTGCGAAGCCTTACGAGAAAGCGG 754



Result No.	Score	Query Match	Length	DB	ID	Description
1	2833	99.4	531	4	US-09-360-197-14	Sequence 14, Appl
2	2447	85.8	533	4	US-09-360-197-10	Sequence 10, Appl
3	1365	47.9	512	2	US-08-828-596-2	Sequence 2, Appl
4	1365	47.9	512	2	US-09-360-197-6	Sequence 6, Appl
5	1337	46.6	559	4	US-09-360-197-8	Sequence 8, Appl
6	1329	46.6	526	4	US-09-360-197-2	Sequence 2, Appl
7	1319	46.3	514	4	US-09-360-197-4	Sequence 4, Appl
8	1249.5	43.8	563	4	US-09-360-197-12	Sequence 12, Appl
9	419	14.7	625	4	US-09-360-197-15	Sequence 15, Appl
10	418.5	14.1	698	1	US-08-376-362A-20	Sequence 20, App
11	403	14.7	564	4	US-09-360-197-16	Sequence 16, App
12	342.5	12.0	493	4	US-09-360-197-4	Sequence 4, Appl
13	341.5	12.0	755	4	US-07-861-458C-99	Sequence 99, Appl
14	338.5	11.9	753	4	US-07-861-458C-98	Sequence 98, Appl
15	320	11.2	520	4	US-07-861-458C-100	Sequence 100, Appl
16	249	8.7	294	6	US-09-337-3-2	Patent No. 5196333-2
17	139	4.9	97	6	US-09-337-3-9	Patent No. 5196333-9
18	127	4.5	13	6	US-09-337-3-6	Patent No. 5196333-6
19	117	4.1	67	6	US-09-337-3-10	Patent No. 5196333-10
20	100.5	3.5	2476	2	US-08-276-967-2	Sequence 2, Appl
21	98	3.4	40	4	US-07-861-458C-118	Sequence 118, Appl
22	97.5	3.4	1051	4	US-09-428-1711A-14	Sequence 14, Appl
23	97	3.4	73	6	US-09-337-3-5	Patent No. 5196333-5
24	94	3.3	422	4	US-08-790-186A-4	Sequence 4, Appl
25	93.5	3.3	582	4	US-09-428-1711A-2	Sequence 2, Appl
26	92.5	3.2	415	4	US-08-795-430-11	Sequence 11, Appl
27	90	3.2	1805	1	US-07-853-913-2	Sequence 2, Appl

28	89.5	3.1	503	4	US-08-959-77A-10	Sequence 10, Appl
29	88	3.1	714	2	US-08-859-201-2	Sequence 2, Appl
30	88	3.1	1102	2	US-08-916-917-4	Sequence 4, Appl
31	88	3.1	1102	2	US-08-972-631-4	Sequence 4, Appl
32	88	3.1	1102	2	US-08-972-629-4	Sequence 4, Appl
33	88	3.1	1102	2	US-08-972-630-4	Sequence 4, Appl
34	88	3.1	1102	2	US-08-972-631-4	Sequence 4, Appl
35	88	3.1	1102	2	US-09-225-170-4	Sequence 4, Appl
36	88	3.1	2539	4	US-09-413-814-42	Sequence 42, Appl
37	86.5	3.0	660	3	US-08-819-177-1	Sequence 1, Appl
38	86	3.0	660	3	US-08-852-153-8	Sequence 8, Appl
39	86	3.0	4150	4	US-09-428-517-2	Sequence 2, Appl
40	85.5	3.0	513	4	US-08-685-558A-18	Sequence 18, Appl
41	85.5	3.0	1043	2	US-08-724-354D-4	Sequence 4, Appl
42	85.5	3.0	1043	2	US-09-770-984A-4	Sequence 4, Appl
43	85.5	3.0	1118	2	US-08-724-354D-2	Sequence 2, Appl
44	85.5	3.0	1118	2	US-09-270-984A-2	Sequence 2, Appl
45	85.5	3.0	3033	1	US-07-925-693-5	Sequence 5, Appl

## ALIGNMENTS

## RESULT 1

```

Sequence 149: Application US/09360197
Patent No. 68250859
GENERAL INFORMATION:
APPLICANT: Bassilana, Frederic
APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Döwelle, Jan R.
TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989.6706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: 09/129,758
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 09/60,095,408
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 531
TYPE: PRT
ORGANISM: Homo sapiens
US-09-360-197-14

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Query Match	Score 2833;	DB 4;	Length 531;
Best Local Similarity	99.74;		
Matches 527; Conservative	99.2;	Pred. No. 9.1e-273;	
	2;	Mismatches 2;	Indels 0; Gaps 0

[illegible]



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Db 186 VFTKYGKCYMNSGDEKPLLTYYKGTGNGLEIMLDIOQDEYLPIMGEBTEETFEAGVK 245
Oy 239 VOIHSQEBPPIIDOLGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPVEEPSPD 298
Db 246 VOIHSQEBPPIIDOLGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPVEEPSPD 298
Oy 299 LGSPSPSPPTTLMGCRACETRYVARKCGCRMYMMPGDVPCSPQOYKNCAPADAI 358
Db 299 -----FPYISITACRIDCETRIVENCNCRMYHMGDAPFCIPBQHKCEAPALGL 350
Oy 359 LKQDS--CACPNPCASTRYAKELSNVRIPSRARAFARKLNRSBAYIAENVLALDIFE 416
Db 351 AEKDSNYCICRCPNLTFRNKELSMVKIPSKTSAKYLEKFKNSKYSISENITLVIDIFE 410
Oy 417 ALNVTYQKRAYEMSELLDIOGOMGLFICASLTIIEILDYCEVRDKYLGIFWNRQ 476
Db 411 ALNVTYQKRAYEVALLDIGOMGLFICASLTIIEILDYCEVRDKYLGIFWNRQ 470
Oy 477 HSQRHSTNLLQEGLSHRTQVPH 500
Db 471 DEGSIDENVSTCDMPNHSITISH 494

```

```

RESULT 4
US-09-360-197-6
; Sequence 6, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Deweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; FILE REFERENCE: 989, 6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-360-197-6

```

```

Query Match 47.9%; Score 1365; DB 4; Length 512;
Best Local Similarity 50.6%; Pred. No. 5.5e-127;
Matches 253; Conservative 83; Mismatches 140; Indels 26; Gaps 5;

```

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Oy 7 PEARROPSDIEVFASNCMSHGLGVFGPSLSLRGMAAAVLSVATFLYQVAREVRY 66
Db 7 PSESSLGSSIOIFANTSTHIGIRIIFVYGLTIRRVLMAAVAFVSLGILLVSESSERYX 66
Oy 67 YREFHQTALDERESHRLVPAVTLCLNINPLRRSLTPNDLHMAGSALLGID-----PAE 121
Db 67 YFSYQHTVKEDEVVAQSLVFPATVCLNINLNGFRFSRLTNDLYHAGELLALLDVLNLIQIPR 126
Oy 122 HAA---FLRAGLRPPAPRGFMSPFEDMAQLYARAGSHSDMLDCCRPRGCGCEBENFTT 178
Db 127 HLAADSVLEALRQKANKFKHYKPK-QFSMLEFLHRVGHDLKCKFKRGQCGHODFTT 185
Oy 179 IFTRMGKCYTFNSGADGAELITTRGGMNGLDIMLVQOQEEYLPVWRNDEETPREVGIR 238
Db 166 VFTKYGKCYMNSGDEKPLLTYYKGTGNGLEIMLDIOQDEYLPIMGEBTEETFEAGVK 245
Oy 239 VOIHSQEBPPIIDOLGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPVEEPSPD 298
Db 246 VOIHSQEBPPIIDOLGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPVEEPSPD 298

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Oy 299 LGSPSPSPPTTLMGCRACETRYVARKCGCRMYMMPGDVPCSPQOYKNCAPADAI 358
Db 299 -----FPYISITACRIDCETRIVENCNCRMYHMGDAPFCIPBQHKCEAPALGL 350
Oy 359 LKQDS--CACPNPCASTRYAKELSNVRIPSRARAFARKLNRSBAYIAENVLALDIFE 416
Db 351 AEKDSNYCICRCPNLTFRNKELSMVKIPSKTSAKYLEKFKNSKYSISENITLVIDIFE 410
Oy 417 ALNVTYQKRAYEMSELLDIOGOMGLFICASLTIIEILDYCEVRDKYLGIFWNRQ 476
Db 411 ALNVTYQKRAYEVALLDIGOMGLFICASLTIIEILDYCEVRDKYLGIFWNRQ 470
Oy 477 HSQRHSTNLLQEGLSHRTQVPH 500
Db 471 DEGSIDENVSTCDMPNHSITISH 494

```

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RESULT 5
US-09-360-197-8
; Sequence 8, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Deweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; FILE REFERENCE: 989, 6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 559
; TYPE: PRT
; ORGANISM: rattus sp.
US-09-360-197-8

```

```

Query Match 46.9%; Score 1337; DB 4; Length 559;
Best Local Similarity 49.8%; Pred. No. 3.8e-124;
Matches 256; Conservative 82; Mismatches 142; Indels 34; Gaps 7;

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Oy 1 MKPTSGPEARQPSDIRFASNCMSHGLGVFGPSLSLRGMAAAVLSVATFLYQV 60
Db 47 MARGSELDEBGDSDPRDIAFAFASCTFHGASHVYFVGCGPRKALMAVAFIALGAFLEQV 106
Oy 61 AERVRYREFHQTALDERESHRLVPAVTLCLNINPLRRSLTPNDLHMAGSALLGIDPA 120
Db 107 GBRVAYLYSPHVTLLDEAVATTELVEFPATVFCNTAVRLSOLSTDYLLT-APMLGLDES 165
Oy 121 EHAALRLAGLRPPAPRGFMSPFEDMAQLYARAGSHSDMLDCCRPRGCGCEBENFTTIF 180
Db 166 DDPGVPLA---PPGEAFSGEP-FNLHFRYNSCHRLEMDLLCYCGPCGPHNFSYVF 221
Oy 181 TFMGKCYTFNSGADGAELITTRGGMNGLDIMLVQOQEEYLPVWRNDEETPREVGIRQ 240
Db 222 TRYGCYTFNSGQDGRPRPKTKMGGTGNGLEIMLDIOQDEYLPVWGETDSFEAGIRVQ 281
Oy 241 IHSQEBPPIIDOLGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPVEEPSPDGL 300
Db 282 IHSQEBPPIIDOLGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPVEEPSPDGL 332
Oy 301 SPSPPSPPTTLMGCRACETRYVARKCGCRMYMMPGDVPCSPQOYKNCAPADAIIR 360
Db 333 -----FDSYSTACRIDCETRIVENCNCRMYHMGDAPCYTPROVECAADPALDIVE 386
Oy 361 KDS--CACPNPCASTRYAKELSNVRIPSRARAFARKLNRSBAYIAENVLALDIFEAL 418

```

Db 387 KDOEYCVCEMPCNLTJRKGELSMVKIPSKASAKYLAKKFNKSEYOIGENILVLIDIFFEVL 446  
Qy 419 NYETEOKKAYEMSELGIDGOMGLFTGASLTLTLETLIDLYCEFRDKVLGYEFMNRQHS 478  
Db 447 NYETEOKKAYEIGLGLGIDGOMGLFTGASLTLVLELFDYAYEYIKHRLC----RRGKC 502  
Qy 479 QRHSSTNLQEGLSHRTQVPHLSLGRPPPTPC 512  
Db 503 QKEAKRSSADKQVA-----LSLDVYKRHNPC 528

RESULT 6  
US-09-360-197-2

; Sequence 2, Application US/09360197  
; Patent No. 6287859  
; GENERAL INFORMATION:  
; APPLICANT: Bassiliana, Frederic  
; APPLICANT: Lazdunski, Michel  
; APPLICANT: Waldmann, Rainer  
; APPLICANT: Deweille, Jan R.  
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive  
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications  
; FILE REFERENCE: 989, 6706P  
; CURRENT APPLICATION NUMBER: US/09/360,197  
; CURRENT FILING DATE: 1997-07-23  
; PRIOR APPLICATION NUMBER: 09/129,758  
; PRIOR FILING DATE: 1998-08-05  
; PRIOR APPLICATION NUMBER: 60/095,408  
; PRIOR FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: rattus sp.  
US-09-360-197-2

Query Match 46.6%; Score 1329; DB 4; Length 526;  
Best Local Similarity 49.5%; Pred. No. 2,1e-123;  
Matches 257; Conservative 79; Mismatches 127; Indels 56; Gaps 8;

Qy 13 QPSDIRVFASNCMHGCHVFGPGSLSLRGMAAAYVLSVATFLYQVAERYRYREFNHQ 72  
Db 14 QPSIOAFASSTLHGMAHIFSYERLSKRALMALCFGLSLAVLLCVCTERYQYFHYHNV 73  
Qy 73 QTALEDERSHRLVPAVTLNINPLRBSRLTPNDLHMGs--ALLG----- 116  
Db 74 VTKIDEVAASQLTFRPATVLCNLNFRFSQVSKNDLYHAGELLALNNRYETPTQMADEK 133  
Qy 117 LDPAEHAFLRALGRPPAPGFMSPPTDMAOLYARAGHSLDMLDCFRGCPGCPEN 175  
Db 134 QLETLQDKANFRS-----FKPKP-FNMREFYDRAGHDIRMLLSCHRGVCSAED 183  
Qy 176 FTTFTRMGKCTYFNSGADGAELETTTRGGMNGCLDMLDVQOEYLYPMWRNDETPFEV 235  
Db 184 FKVFTRYGKCTYFNSGADGAPRLTKTMKGNGLEMLDIOODEYLYPMWGETDETSTFEA 243  
Qy 236 GIRVOIHSOEPRITDOLGLVSPGYOTFYSCQOOLSFLLPPMGDCSSALNPNYEPER 295  
Db 244 GIRVOIHSODEPRITDOLGLVAGFOTFYSCQOOLILYLPSPMGTCNATYMDSDF---- 299  
Qy 296 SDPLGSPSPSPPYTLMGCRACETRYVARKCCGRMYVMBGDVPCSPQOYKNCANPAID 355  
Db 300 -----FDSYSTRACRIDCETRYLVENCRCRMVHMGDAPYCTPEQYKCADPALD 348  
Qy 356 DALIRKDS--CACRNPASRYAKELSMVRIIPRAAARFLARKLNREAYIAENVLALDI 413  
Db 349 DFLVEKDQEXCVCEMPCNLTJRKGELSMVKIPSKASAKYLAKKFNKSEYOIGENILVLDI 408  
Qy 414 FFEALNTEYEOKKAYEMSELGIDGOMGLFTGASLTLTLETLIDLYCEFRDKVLGYFM 473  
Db 409 FFEVLTNETIEOKKAYEIGLGLGIDGOMGLFTGASLTLVLELFDYAYEYIKHRLC---- 464

Qy 474 NROHSQRHSSTNLQEGLSHRTQVPHLSLGRPPPTPC 512  
Db 465 RRGKQKRAKRSADKQVA-----LSLDVYKRHNPC 495

## RESULT 7

US-09-360-197-4

; Sequence 4, Application US/09360197  
; Patent No. 6287859  
; GENERAL INFORMATION:  
; APPLICANT: Bassiliana, Frederic  
; APPLICANT: Lazdunski, Michel  
; APPLICANT: Waldmann, Rainer  
; APPLICANT: Deweille, Jan R.  
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive  
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications  
; FILE REFERENCE: 989, 6706P  
; CURRENT APPLICATION NUMBER: US/09/360,197  
; CURRENT FILING DATE: 1997-07-23  
; PRIOR APPLICATION NUMBER: 09/129,758  
; PRIOR FILING DATE: 1998-08-05  
; PRIOR APPLICATION NUMBER: 60/095,408  
; PRIOR FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 514  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-360-197-4

Query Match 46.3%; Score 1319; DB 4; Length 514;  
Best Local Similarity 49.2%; Pred. No. 2e-122;  
Matches 255; Conservative 80; Mismatches 129; Indels 54; Gaps 8;

Qy 14 PSDIRVFASNCMHGCHVFGPGSLSLRGMAAAYVLSVATFLYQVAERYRYREFNHQ 73  
Db 1 PVSIOAFASSTLHGMAHIFSYERLSKRALMALCFGLSLAVLLCVCTERYQYFHYHNV 60  
Qy 74 TALEDERSHRLVPAVTLNINPLRBSRLTPNDLHMGs--ALLG----- 116  
Db 61 TKLDEVAASQLTFRPATVLCNLNFRFSQVSKNDLYHAGELLALNNRYETPTQMADEK 120  
Qy 117 LDPAEHAFLRALGRPPAPGFMSPPTDMAOLYARAGHSLDMLDCFRGCPGCPEN 176  
Db 121 LEIQLQDKANFRS-----FKPKP-FNMREFYDRAGHDIRMLLSCHRGVCSAED 170  
Qy 177 TTTFTRMGKCTYFNSGADGAELETTTRGGMNGCLDMLDVQOEYLYPMWRNDETPFEV 236  
Db 171 KVFTRYGKCTYFNSGNGRPRRLTKTMKGNGLEMLDIOODEYLYPMWGETDETSTFEAG 230  
Qy 237 IRVOIHSOEPRITDOLGLVSPGYOTFYSCQOOLSFLLPPMGDCSSALNPNYEPER 296  
Db 231 IKVOIHSODEPRITDOLGLVAGFOTFYVACQOOLILYLPSPMGTCNATYMDSDLFDS 290  
Qy 297 DPLGSPSPSPPYTLMGCRACETRYVARKCCGRMYVMBGDVPCSPQOYKNCANPAID 356  
Db 291 -----YSITACRIDCETRYLVENCRCRMVHMGDAPYCTPEQYKCADPALD 337  
Qy 357 AILRKDS--CACRNPASRYAKELSMVRIIPRAAARFLARKLNREAYIAENVLALDI 414  
Db 338 FLVEKDQEXCVCEMPCNLTJRKGELSMVKIPSKASAKYLAKKFNKSEYOIGENILVLDI 397  
Qy 415 FFEALNTEYEOKKAYEMSELGIDGOMGLFTGASLTLTLETLIDLYCEFRDKVLGYFM 474  
Db 398 FEVLTNETIEOKKAYEIGLGLGIDGOMGLFTGASLTLVLELFDYAYEYIKHRLC----R 453  
Qy 475 ROHSQRHSSTNLQEGLSHRTQVPHLSLGRPPPTPC 512  
Db 454 RRGKQKRAKRSADKQVA-----LSLDVYKRHNPC 483

## RESULT 8

US-09-360-197-12  
; Sequence 12, Application US/09360197  
; Patent No. 6287859  
; GENERAL INFORMATION:  
; APPLICANT: Bassilana, Frederic  
; APPLICANT: Lazdunski, Michel  
; APPLICANT: Waldmann, Rainer  
; APPLICANT: Deweille, Jan R.  
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive  
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications  
; FILE REFERENCE: 989.6706P  
; CURRENT APPLICATION NUMBER: US/09/360.197  
; CURRENT FILING DATE: 1997-07-23  
; PRIOR APPLICATION NUMBER: 09/129,758  
; PRIOR FILING DATE: 1998-08-05  
; PRIOR APPLICATION NUMBER: 60/095,408  
; PRIOR FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 563  
; TYPE: PRT  
; ORGANISM: ratus sp.  
US-09-360-197-12  
Query Match 43.8%; Score 1249.5; DB 4; Length 563;  
Best Local Similarity 47.5%; Pred. No. 1.9e-115;  
Matches 245; Conservative 79; Mismatches 151; Indels 41; Gaps 8;  
QY 6 GGEARR-OPSDIRVAFASNCMHGLGV---FGPGSLIRGMAAAVLSVATFLYQV 60  
DB 50 GGVAVRGRPS-----LSRTKLHGLRHMCAGRTAAGSGQRALAVLAFCTSLGLLSMS 104  
QY 61 AERVATYREFHHQTLADRESHRLVPRVATLCINPRLRSRLTPNDLHAGSALLGLDPA 120  
DB 105 SNRLLYWLSFSPHTRVHREMSRQLPFPVATYCNPNPRLRPSKGLDYAGHMLGILLFN 164  
QY 121 EHA-AFLRALGRPARPG-----FMPSPTFD--MAQLYARAGSHLDMILDCRF 166  
DB 165 RYARLVSESLRGDEPRRQWFRKLADFLFLPRHREGISAFFMDLGHQLEDMLLSCKY 224  
QY 167 RGQPCGPNFTTITRMGKCYTFNSGADGAEILLTTTGGMGNGLDMIDVOOEYLPVR 226  
DB 225 RQELGPHNFSVFTKYGKCYFMNSGDEGKPLTTVKGSTGNGLEIMDIQODEVTLPIWG 284  
QY 227 DNEETPEFVGIVQIHSQDEPPIIDQLGVSPTGYQTFVSCQOOLSLFPPWDCSSAS 286  
DB 285 ETEETTFEAGVYQIHSQSEPPFIQELGFGVAPGFOTFVATQEORLTYLPPWGECSSE 344  
QY 287 LNPNTPEPSDPLGSPSPSPRYTLMGCRLCETRYVARKCGCMYVMPGDPVPCSPQ 346  
DB 345 MGLD-----FPVYSITACRIDCETRYIENCGRYVHPGAPCTPPO 389  
QY 347 YKNCAPAIADILARKDS--CACPNPCASTRYAKELSMVRIPIRAARAFIARKLNSEAVI 404  
DB 390 HKECAPRALGLIAEKDSNVCICRTPCNLTTRYKELSMVRIPIRTAKYIEKKFNSEKI 449  
QY 405 AENVIALDIFFPALYETVEOKKAYEMSELLDGGOMGLTGASILLTLELDYLCVEY 464  
DB 450 SENIILVLDIFFEALNYETIEOKKAYEVALLDGIGOMGLTGASILLTLELDYIELI 509  
QY 465 RDKVLGYFMNRHQSRRHSSTNLQGLGSHRTQVPH 500  
DB 510 KEKLIDLGLKEEESGHDENNSTCDTPMNHSETTISH 545

RESULT 9  
US-09-360-197-15  
; Sequence 15, Application US/09360197  
; Patent No. 6287859  
; GENERAL INFORMATION:  
; APPLICANT: Bassilana, Frederic  
; APPLICANT: Lazdunski, Michel  
US-09-360-197-15  
Query Match 14.7%; Score 419; DB 4; Length 625;  
Best Local Similarity 22.2%; Pred. No. 6.7e-33;  
Matches 136; Conservative 99; Mismatches 191; Indels 186; Gaps 20;  
QY 17 IRVFASNCMHGLGVFGPGSLIRGMAAAVLSVATFLYQVAREVRYREFHHQTL 76  
DB 43 IAEIGSESNHGLAKIVTSRD-TKKRVIALLVIGFTATITQLSLVRKYLQFVVELS 101  
QY 77 DERESHRLVPRVATLCINP-----LRR--SRLTPNDLHAGSALLGLDPAEHAFLRA 128  
DB 102 EIKDSMPVQYFVSSICINIPISLRTIRMYFNNESSQNTLWTL--RFIOKFEEDOSFMS 159  
QY 129 LGRPARPFGFMSPTF--MAQLYARAGSHLDMILDCRFROGCPGPNFTTITF-RMK 185  
DB 160 I-----RAVEMLGODAKKLSHLEDMLHCFNRELCHVSNFSTFFGQNFN 207  
QY 186 CYTFNSGADGAEILLTTTGGMGNGLDMIDVOOEYLP-----VMDNEETPREVGIRVOI 241  
DB 208 CTFPNS-----QRLQMHANCPENGSLISFVEKDEPLPCTGYVYNDNLIHSAGVRYV 263  
QY 242 HSOEPPPIIDQLGVSPTGYQTFVSCQOOLSLFPPWDCSSASLN--PNYEPEPSDPL 299  
DB 264 HAPGSPSPFVDHIGIDIPPGYSSVGLKAILHTRLPYPGNCNDMLNGIKQYK----- 316  
QY 300 GSPSPSPRYTLMGCRLCETRYVARKCGCMYVMPGVP----- 340  
DB 317 -----YTFACLOLCKQRLIIQRCGCKSSALP-EVPSYNAFTFCGVIKDQWEINRN 365  
QY 341 -----VCSPQOYKNCAPAIADILARKD-----SCAPNPCASTR 374  
DB 366 HSNEDHNOSEEDRAFIPTYIACEREOKN-----LNDRIYELSCGFCQFCSETS 416  
QY 375 YAKELSMWRIP-----SRAARFIARKLNSEAVI----- 405  
DB 417 YLKSYSLSWPLFEYQLSAVERFQEOBQAGNHFKAYEYLEKLAHPSQHLARNDSH 476  
QY 406 -----ENVIALDIFFPALYETVEOKKAYEMSELLDGGOMGLTGASILLTLELDY 440  
DB 477 MDDLISKYSYLSSEKEMAKASDLIRQNMRLNLYIEDLSVEYEROLPAYGLADLPADJGG 536  
QY 441 OMGLFGASILLTLELDYLCVEFVRDYLGYFMNRQ-----HSQRHS 482  
DB 537 TGLMKGISVILIMELIELYI-----RLTGLVFNSEKGLRPGPTVYNNNGSNHNSQ-ST 590  
QY 483 STNLLQEGIGSH 494  
DB 591 SQHQLYNGYMDH 602

RESULT 10  
US-08-376-362A-20  
; Sequence 20, Application US/08376362A  
; Patent No. 5693756  
; GENERAL INFORMATION:





```

; APPLICANT: Johnson, Carl D.
; TITLE OF INVENTION: HOMOLOG CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861,458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753
; TYPE: amino acid
; TOPOLOGY: linear
;
US-07-861-458C-98
Query Match 11.9%; Score 338.5; DB 4; Length 753;
Best Local Similarity 27.2%; Pred. No. 8.9e-25;
Matches 106; Conservative 56; Mismatches 137; Indels 91; Gaps 14;

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; Patent No. 6232061
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark Andrew
; TITLE OF INVENTION: HOMOLOG CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861,458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520
; TYPE: amino acid
; TOPOLOGY: linear
;
US-07-861-458C-100
Query Match 11.2%; Score 320; DB 4; Length 520;
Best Local Similarity 22.2%; Pred. No. 3.5e-23;
Matches 121; Conservative 61; Mismatches 178; Indels 184; Gaps 19;

```



Db 393 AINFNIGADCPAYVHIISNDKACAEYRRLNTAYIEIYEQINFEYTLKETAGYTLVNLPSD 452  
QY 438 IGGOMGLFIFIGASLFTLIEILDYLCFV-----FRDKVLGYFPWNRQHSQHSSTN 485  
Db 453 FCGNIGIMIGFSVYTMFEVVEVLCEIITYIGTHSLFKLFSKLL-----PSQENNHATA 505  
QY 486 LLOE 489  
Db 506 FINE 509

Search completed: October 11, 2002, 08:11:12  
Job time : 35 secs





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Db 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFGQPCGPENFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPEFVGIRVQ 240
Db 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPEFVGIRVQ 240
OY 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOISFLPPWGDSSASLNPNEPEPSDPLG 300
Db 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOISFLPPWGDSSASLNPNEPEPSDPLG 300
OY 301 SPSPSPSPPTLMGCRCLACETRYVARKCGCRMYMPGVPCSPQOYKNCAHPAIDALIR 360
Db 301 SPSPSPSPPTLMGCRCLACETRYVARKCGCRMYMPGVPCSPQOYKNCAHPAIDALIR 360
OY 361 KDSQCAPPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
Db 361 KDSQCAPPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
OY 421 ETEQCKKAYEMSELLDGGOMGLFTGASLLTILEILDYLCVEFRDKVLGYFWRNQSQR 480
Db 421 ETEQCKKAYEMSELLDGGOMGLFTGASLLTILEILDYLCVEFRDKVLGYFWRNQSQR 480
OY 481 HSTNLLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLVTOI 531
Db 481 HSTNLLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLVTOI 531

```

## RESULT 2

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OY 09098 PRELIMINARY: PRT: 531 AA.
AC 09098:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTON-GATED CATION CHANNEL ASIC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96416055; PubMed=9744806;
RA de Weille J.R., Bassilana F., Lazdunski M., Waldmann R.;
RT "Identification, functional expression and chromosomal localisation of
RT a sustained human proton-gated cation channel.";
RL FEBS Lett. 433:257-260(1998);
DR EMBL; AF095897; AAC64188.1;
DR InterPro; IPR001873; ASC.
DR Pfam; PF00858; ASC.
DR PRINTS; PRO1078; AMINCHANNEL.
SQ SEQUENCE 531 AA; 58905 MW; A46DD64590EC4871 CRC64;

```

## Query Match

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Best Local Similarity 99.28; Score 2833; DB 4; Length 531;
Pred. No. 1.4e-251;
Matches 527; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY 1 MKPTSGPEARROPDSIDIVFASNCMGLGVFGPSTSLRGMMAAAVLSVATFLYQV 60
Db 1 MKPTSGPEARROPDSIDIVFASNCMGLGVFGPSTSLRGMMAAAVLSVATFLYQV 60
OY 61 AERYVYREFHQTALDERESHRLVPAVTLCTNINPLRRSLTTPNDLHMAGSALLGLDPA 120
Db 61 AERYVYREFHQTALDERESHRLVPAVTLCTNINPLRRSLTTPNDLHMAGSALLGLDPA 120
OY 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFGQPCGPENFTTIF 180
Db 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFGQPCGPENFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPEFVGIRVQ 240
Db 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPEFVGIRVQ 240
OY 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOISFLPPWGDSSASLNPNEPEPSDPLG 300

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Db 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOISFLPPWGDSSASLNPNEPEPSDPLG 300
OY 301 SPSPSPSPPTLMGCRCLACETRYVARKCGCRMYMPGVPCSPQOYKNCAHPAIDALIR 360
Db 301 SPSPSPSPPTLMGCRCLACETRYVARKCGCRMYMPGVPCSPQOYKNCAHPAIDALIR 360
OY 361 KDSQCAPPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
Db 361 KDSQCAPPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
OY 421 ETEQCKKAYEMSELLDGGOMGLFTGASLLTILEILDYLCVEFRDKVLGYFWRNQSQR 480
Db 421 ETEQCKKAYEMSELLDGGOMGLFTGASLLTILEILDYLCVEFRDKVLGYFWRNQSQR 480
OY 481 HSTNLLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLVTOI 531
Db 481 HSTNLLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLVTOI 531

```

## RESULT 3

```

ID 060263 PRELIMINARY: PRT: 532 AA.
AC 060263:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SODIUM CHANNEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=96238685; PubMed=95711199;
RA Ishibashi K., Marumo F.;
RT "Molecular cloning of a DEG/ENAC sodium channel cDNA from human
RT testis";
RL Biochem. Biophys. Res. Commun. 245:589-593(1998).
DR EMBL; AB010575; BAA25897.1;
DR InterPro; IPR001873; ASC.
DR Pfam; PF00858; ASC.
SQ SEQUENCE 532 AA; 59154 MW; B84CB4A1ACAD02FB CRC64;

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## Query Match

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Best Local Similarity 97.18; Score 2768.5; DB 4; Length 532;
Pred. No. 1.2e-245;
Matches 516; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

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OY 1 MKPTSGPEARROPDSIDIVFASNCMGLGVFGPSTSLRGMMAAAVLSVATFLYQV 60
Db 1 MKPTSGPEARROPDSIDIVFASNCMGLGVFGPSTSLRGMMAAAVLSVATFLYQV 60
OY 61 AERYVYREFHQTALDERESHRLVPAVTLCTNINPLRRSLTTPNDLHMAGSALLGLDPA 120
Db 61 AERYVYREFHQTALDERESHRLVPAVTLCTNINPLRRSLTTPNDLHMAGSALLGLDPA 120
OY 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFGQPCGPENFTTIF 180
Db 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFGQPCGPENFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPEFVGIRVQ 240
Db 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPEFVGIRVQ 240
OY 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOISFLPPWGDSSASLNPNEPEPSDPLG 300
Db 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOISFLPPWGDSSASLNPNEPEPSDPLG 300
OY 301 SPSPSPSPPTLMGCRCLACETRYVARKCGCRMYMPGVPCSPQOYKNCAHPAIDALIR 359
Db 301 SPSPSPSPPTLMGCRCLACETRYVARKCGCRMYMPGVPCSPQOYKNCAHPAIDALIR 360

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OY 360 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFEEALN 419
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DB 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFEEALN 420
OY 420 YETVEOKKAYEMSELGIDIGOMGLFTIGASLLTLEILDYLCVEFRDKVLGYFNNRQHSQ 479
    |||||||
DB 421 YETVEOKKAYEMSELGIDIGOMGLFTIGASLLTLEILDYLCVEFRDKVLGYFNNRQHSQ 480
OY 480 RRSSTNLQEGLSGSHRTQVPHLSLGRPPPTPCAVTKTLSASHRTCYLTOL 531
    |||||||
DB 481 RRSSTNLQEGLSGSHRTQVPHLSLGRPPPTPCAVTKTLSASHRTCYLTOL 532

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## RESULT 4

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OY 090HC3 PRELIMINARY: PRT; 549 AA.
AC 090HC3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACID SENSING ION CHANNEL 3 SPLICE VARIANT C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Renard S., Besnard F., Partiseti M., Graham D.;
RT ASIC3b, a new member of the acid sensing ion channel family.";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF195025; AAF19818.1; -
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PRINTS: PRO1078; AMINACHANNEL.
SQ SEQUENCE 549 AA; 60491 MW; ED2C4D628AF9E18F CRC64;

```

Query Match 94.9%; Score 2706; DB 4; Length 549;

Best Local Similarity 93.9%; Pred. No. 6,7e+240;

Matches 511; Conservative 3; Mismatches 14; Indels 16; Gaps 2;

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OY 1 MKPTSGPEBARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMAAAVYLVSATFLYOV 60
    |||||||
DB 1 MKPTSGPEBARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMAAAVYLVSATFLYOV 60
OY 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNDLHMAGSALLGIDPA 120
    |||||||
DB 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNDLHMAGSALLGIDPA 120
OY 121 EHAALFALGRPPAPPGFMPSPFTDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
    |||||||
DB 121 EHAALFALGRPPAPPGFMPSPFTDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
OY 121 EHAALFALGRPPAPPGFMPSPFTDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
    |||||||
DB 121 EHAALFALGRPPAPPGFMPSPFTDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGLDIMLDVQOEYLLPVWRDNEETPREVGIRVO 240
    |||||||
DB 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGLDIMLDVQOEYLLPVWRDNEETPREVGIRVO 240
OY 241 IHSQEBPPIIDQGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPYEPEPSDPLG 300
    |||||||
DB 241 IHSQEBPPIIDQGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPYEPEPSDPLG 300
OY 301 SPSPSPPTTLMGCLACETRIVYARKCGCRMVYMGDVPVCSPOOYKNCAPHAIDAILR 360
    |||||||
DB 301 SPSPSPPTTLMGCLACETRIVYARKCGCRMVYMGDVPVCSPOOYKNCAPHAIDAILR 360
OY 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFEEALN 420
    |||||||
DB 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFEEALN 420
OY 421 EYVEOKKAYEMSELGIDIGOMGLFTIGASLLTLEILDYLCVEFRDKVLGYFNNRQHSQ 480
    |||||||
DB 421 EYVEOKKAYEMSELGIDIGOMGLFTIGASLLTLEILDYLCVEFRDKVLGYFNNRQHSQ 480
OY 481 HSTNLTSLQEGLSGSHRTQVPHLSLGR-----PP-----TPPCAVTKTLSASHRT 524

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DB 481 HSTNLTSLQEGLSGSHRTQVPHLSLGRPSTLLCSEDLPLVPVSPRLSPPTPARATLSSSRP 540
    |||||||
OY 525 CYLV 528
    ||
DB 541 AVCV 544

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## RESULT 5

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OY 090HC4 PRELIMINARY: PRT; 543 AA.
AC 090HC4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ACID SENSING ION CHANNEL 3 SPLICE VARIANT B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Renard S., Besnard F., Partiseti M., Graham D.;
RT ASIC3b a new modulatory subunit of the acid sensing ion channel
RT family.";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF195024; AAF19817.1; -
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PRINTS: PRO1078; AMINACHANNEL.
SQ SEQUENCE 543 AA; 60331 MW; 9411BD1485BA93F1 CRC64;

```

Query Match 91.1%; Score 2598; DB 4; Length 543;

Best Local Similarity 93.9%; Pred. No. 5,5e+230;

Matches 491; Conservative 4; Mismatches 12; Indels 16; Gaps 3;

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OY 1 MKPTSGPEBARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMAAAVYLVSATFLYOV 60
    |||||||
DB 1 MKPTSGPEBARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMAAAVYLVSATFLYOV 60
OY 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNDLHMAGSALLGIDPA 120
    |||||||
DB 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNDLHMAGSALLGIDPA 120
OY 121 EHAALFALGRPPAPPGFMPSPFTDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
    |||||||
DB 121 EHAALFALGRPPAPPGFMPSPFTDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGLDIMLDVQOEYLLPVWRDNEETPREVGIRVO 240
    |||||||
DB 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGLDIMLDVQOEYLLPVWRDNEETPREVGIRVO 240
OY 241 IHSQEBPPIIDQGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPYEPEPSDPLG 300
    |||||||
DB 241 IHSQEBPPIIDQGLGVSPGYOTFVSCQOQOLSFLLPPMGDCSSASINPYEPEPSDPLG 300
OY 301 SPSPSPPTTLMGCLACETRIVYARKCGCRMVYMGDVPVCSPOOYKNCAPHAIDAILR 360
    |||||||
DB 301 SPSPSPPTTLMGCLACETRIVYARKCGCRMVYMGDVPVCSPOOYKNCAPHAIDAILR 360
OY 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFEEALN 420
    |||||||
DB 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFEEALN 420
OY 421 EYVEOKKAYEMSELGIDIGOMGLFTIGASLLTLEILDYLCVEFRDKVLGYFNNRQHSQ 480
    |||||||
DB 421 EYVEOKKAYEMSELGIDIGOMGLFTIGASLLTLEILDYLCVEFRDKVLGYFNNRQHSQ 480
OY 481 HSTNLTSLQEGLSGSHRTQV---PHL-----SLGPP 507
    |||||||
DB 481 HSTNLTSLQEGLSGSHRTQV---PHL-----SLGPP 507

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RESULT 6  
ID 035240 PRELIMINARY; PRT; 533 AA.  
AC 035240;  
DT 01-JAN-1998 (Tremblrel. 05, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE PROTON GATED CATION CHANNEL DRASIC.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97407870; PubMed=9261094;  
RA Weidmann R., Bassilana F., de Weille J., Champigny G., Heurteaux C., Lazdunski M.;  
RT "Molecular cloning of a non-inactivating proton-gated Na<sup>+</sup> channel  
specific for sensory neurons."  
RL J. Biol. Chem. 272:20975-20978(1997).  
DR EMBL; AF013598; AAB69328.1;  
DR InterPro; IPR001873; ASC.  
DR Pfam; PF00858; ASC.1.  
SQ SEQUENCE 533 AA; 59226 MW; 294B57322C74B3DC CRC64;  
Query Match 445; Score 2447; DB 11; Length 533;  
Best Local Similarity 488.5%; Pred. No. 4e-216;  
Matches 445; Conservative 49; Mismatches 37; Indels 2; Gaps 2;  
QY 1 MKPTSGPEEA-RROPSDTRVNASNMGHGVFGPSLSLRGMAAAYLVSVATELYQ 59  
DB 1 MKPRGEEAORROASDIRVASSCTMIGHIFGPGGLTRRGMAVAVALLSLAFLYQ 60  
QY 60 VAERARYREFHQTALDERESHRLVPAYVLCININPLRKRSLTPNDLHMAGSALLGDP 119  
DB 61 VAERARYGEGHHTKTLDERSHOLTTPAYVLCININPLRKRSLTPNDLHMAGTALGDP 120  
QY 120 AEHAFLRALGRPARPGFMSPPTDMAOLYARAGSLDMLDCRFRGOCGPENFTT 179  
DB 121 AEHAAYLRALGQPARPGFMSPPTDMAOLYARAGSLDMLDCRFRGOCGPENFTVI 180  
QY 180 FTRRGKCTFNSGADGALLTTTRGKMGNGDLMIDVOOEYLPVRNDETFPEVGRV 239  
DB 181 FTRRGQCTFNSGAGALLTTTRGKMGNGLEIMLDVVOEYLPVRNDETFPEVGRV 240  
QY 240 QIHSEBEPITDQGLGVSFGYOTFVSCQOQQLSFLPPMGDCSSANP-NYEPEDP 298  
DB 241 QIHSDDEPITDQGLGFGARPGHGTFSQOQQLSFLPPMGDCNATASLDPDFDEPDP 300  
QY 299 LGSPPSPSPPYTLMGCRACETRIVARCGCRMVMPGDVPCSPQOYKNCAPALDAI 358  
DB 301 LGSPPSPSPPYTLMGCRACETRIVARCGCRMVMPGDVPCSPQOYKNCAPALDAM 360  
QY 359 LKRSACPNACSTRYAKELSMVRIPSRARAFARLNSEAYIAENVLALDIEFFAL 418  
DB 361 LKRDTCVPCNCASTRYAKELSMVRIPSRARAFARLNSEAYIAENVLALDIEFFAL 420  
QY 419 NYETVEOKKAAEMSELDDIGOMGLFGASLTLTLELDVCEFRDVKLYGFENRHS 478  
DB 421 NYEAVEOKKAAEVESELDDIGOMGLFGASLTLTLELDVCEFRDVKLYGFENRHS 480  
QY 479 QHRSSTNLQEGLSHRTQVPHLSLGRPPPCAVTKTSLASHRTCYLVQ 531  
DB 481 QHRSSTNLQEGLSHRTQVPHLSLGRPPPCAVTKTSLASHRTCYLVRL 533

RESULT 7  
ID 0925H0 PRELIMINARY; PRT; 512 AA.  
AC 0925H0;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE BRAIN SODIUM CHANNEL 1 ALPHA SUBUNIT.  
GN ACCN1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C;  
RX MEDLINE=97188490; PubMed=9037075;  
RA Garcia-Anoveros J., Derfler B., Neville-Golden J., Hyman B.T., Corey D.P.;  
RT "Bnac1 and Bnac2 constitute a new family of human neuronal sodium channels related to degenerins and epithelial sodium channels."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:1459-1464(1997).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C;  
RX MEDLINE=21204130; PubMed=11306621;  
RA Garcia-Anoveros J., Samad T.A., Zuvela-Jelaska L., Woolf C.J., Corey D.P.;  
RT "Transport and Localization of the DEG/ENAC Ion Channel Bnac1alpha to Peripheral Mechanosensory Terminals of Dorsal Root Ganglia Neurons."  
RL J. Neurosci. 21:2678-2686(2001).  
DR EMBL; AF348465; AAK40101.1;  
KW Ionic channel.  
SQ SEQUENCE 512 AA; 57739 MW; 7D81A77C3B347B04 CRC64;  
Query Match 47.9%; Score 1367; DB 11; Length 512;  
Best Local Similarity 50.6%; Pred. No. 6.3e-117;  
Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;  
QY 7 PEARROPSDIRVNASNMGHGVFGPSLSLRGMAAAYLVSVATELYQYAEVRY 66  
DB 7 PSESLQPSISQIRFANSTLGHIRHIFVYGLTRVLMVAFAVGSGLLVESSERSY 66  
QY 67 YREFHQTALDERESHRLVPAYVLCININPLRKRSLTPNDLHMAGSALLGID-----PAE 121  
DB 67 YEFYOHVTKVDEVAQSLVPAYVLCININPLRKRSLTPNDLHMAGSALLGID-----PAE 126  
QY 122 HAA---FLRALGRPARPGFMSPPTDMAOLYARAGSLDMLDCRFRGOCGPENFTT 178  
DB 127 HLADETVLEALROKANKRHYKPK-QFSKLEPLHNVGHDLDKMLYCFKFGQEGCHQDFTT 185  
QY 179 IFTRMGKCTFNSGADGALLTTTRGKMGNGDLMIDVOOEYLPVRNDETFPEVGRV 238  
DB 186 VFTKYGKCYMNSGDBDKPLTTVKGNGLEIMLDVVOEYLPVINGETETFEAGVK 245  
QY 239 VQHSQEBEPITDQGLGVSFGYOTFVSCQOQQLSFLPPMGDCSSANPNIYEPEDP 298  
DB 246 VQHSQEBEPITDQGLGVSFGYOTFVSCQOQQLSFLPPMGDCSSANPNIYEPEDP 298  
QY 299 LGSPPSPSPPYTLMGCRACETRIVARCGCRMVMPGDVPCSPQOYKNCAPALDAI 358  
DB 299 LGSPPSPSPPYTLMGCRACETRIVARCGCRMVMPGDVPCSPQOYKNCAPALDAI 358  
QY 359 LKRS--CACPNPCASTRYAKELSMVRIPSRARAFARLNSEAYIAENVLALDIEFF 416  
DB 351 LKRSNVCCLCTPCNLRYNKELSMVRIPSRARAFARLNSEAYIAENVLALDIEFF 410  
QY 417 ALNTEYBOKKAAEMSELDDIGOMGLFGASLTLTLELDVCEFRDVKLYGFENRQ 476  
DB 411 ALNTEYBOKKAAEMSELDDIGOMGLFGASLTLTLELDVCEFRDVKLYGFENRQ 470  
QY 477 HSQRHSTNLQEGLSHRTQVPH 500  
DB 471 EGSQHDENMSTCDTPMNHSETISH 494

RESULT 8  
ID 088762 PRELIMINARY; PRT; 513 AA.  
AC 088762;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ASIC-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9837436; PubMed=9707631;
RA Chen C.C., England S., Akopian A.N., Wood J.N.;
RT "A sensory neuron-specific, proton-gated ion channel."
RL Proc. Natl. Acad. Sci. U.S.A. 95:10240-10245(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
DR EMBL: AJ006519; CAA07080.1;
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 2.
DR PROSITE: PS01206; ASC. 1.
KW Glycoprotein; Ion transport; Ionic channel; Transmembrane.
SQ SEQUENCE 513 AA; 57016 MW; 02100E166E2F32A3 CRC64;

Query Match 47.0%; Score 1340; DB 11; Length 513;
Best Local Similarity 49.8%; Pred. No. 1.9e-114;
Matches 256; Conservative 83; Mismatches 141; Indels 34; Gaps 7;

QY 1 MKPTSGPEEARROPSDIRVAFASCSMHGLGHVGPGLSLRRGMAAAVVLVSATPLXYOV 60
D 1 MEAGSELDEGDDSPRDVLVAFAVANSCTLHGASHVEEGGPGPROMLVAFVIALGAFLCQV 60
QY 61 AERYRYREPHHOTALDERESHRLVPAVYTCINPLRGRSLRPNDLHMAASALLGDPA 120
D 61 GDRVAYILSPHYTLDEVAITSELPVAFCTNNAVRLSOLSYPDLLYL-APMLGIDES 119
DB 61 TRGKCYTFNSGDDGRPRLTMTKGTGNGLEIMLDIOQDEYLPVWGTDSTFEAGIKYQ 180
QY 121 EHAATFALGRPAAPGFMSPFDMAOLYARAGHSLDMLDCRFRGQCGPENFTTIF 180
D 120 DDGCVPLA---PPGEAFSGEP-FNLHRYNRSCHRLIEDMLYCSYCGGCGPHNFSVVF 175
QY 181 TRGKCYTFNSGADGAEELLTTRGKMGNGIDMLDVQOEYLLPVWRNDEETPREVGIRYQ 240
D 176 TRGKCYTFNSGDDGRPRLTMTKGTGNGLEIMLDIOQDEYLPVWGTDSTFEAGIKYQ 235
QY 241 IHSQEEPPITDOLGLGVSPGYOTFVSCQOQOQLFLPRPMWDCSSASLNPVYEEPPSPLG 300
D 236 IHSQDEPPITDOLGLGVAPGFQTFVSCQEQRLLYLPSPWGTCAVYWDSDP----- 286
QY 301 SPSPSPSPPTTLMGCRACETRYVARKCGRMVYMGDVVCSPOOYKNCAPHAIDAIR 360
D 287 -----FDSYSTACRIDCTETRYLVENCNCRMYHMPGDAPYCTPEOYKECADPALDFVE 340
QY 361 KDS--CACPNPCASTRAKELSWRIPSRARARLAKRLRSBAYIAENVLADIFEAL 418
D 341 KDQECVCEMPCNLTGRKELSMVKIPSKASAKYLAKEFKSEQYIGENILVLDIFEVL 400
QY 419 NYETVQKRAYESELGLDGGOMGLFICASLITILEILDYLCVFRDKYLGYFMNRQHS 478
D 401 NYETIEQKRAYETAGLGLDGGOMGLFICASLITILELFDYAEVYIKHRLC---RRGKC 456
QY 479 QRHSSTNLQEGLSHRTQVPHLSLGRPPTPPC 512
D 457 QKEAKRSSADKGYA-----LSLDVKKRHNP 482

RESULT 9
ID 091YB8 PRELIMINARY; PRT; 559 AA.
AC 091YB8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ION CHANNEL.

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GN ASIC 1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX Baessler E.L., Ngo-Anh J., Geisler H.S., Ruppersberg J.P., Grunder S.;
RT "Molecular and functional characterization of acid-sensing ion channel
RT (ASIC) 1b."
RL J. Biol. Chem. 276:33783-33787(2001).
DR EMBL: AJ309926; CAC44267.1;
SQ SEQUENCE 559 AA; 62217 MW; 0F438117B95C18E5 CRC64;

Query Match 47.0%; Score 1339; DB 11; Length 559;
Best Local Similarity 49.8%; Pred. No. 2.7e-114;
Matches 256; Conservative 83; Mismatches 141; Indels 34; Gaps 7;

QY 1 MKPTSGPEEARROPSDIRVAFASCSMHGLGHVGPGLSLRRGMAAAVVLVSATPLXYOV 60
D 47 MEAGSELDEGDDSPRDVLVAFAVANSCTLHGASHVEEGGPGPROMLVAFVIALGAFLCQV 106
QY 61 AERYRYREPHHOTALDERESHRLVPAVYTCINPLRGRSLRPNDLHMAASALLGDPA 120
D 107 GDRVAYILSPHYTLDEVAITSELPVAFCTNNAVRLSOLSYPDLLYL-APMLGIDES 165
QY 121 EHAATFALGRPAAPGFMSPFDMAOLYARAGHSLDMLDCRFRGQCGPENFTTIF 180
D 166 DDGCVPLA---PPGEAFSGEP-FNLHRYNRSCHRLIEDMLYCSYCGGCGPHNFSVVF 221
QY 181 TRGKCYTFNSGADGAEELLTTRGKMGNGIDMLDVQOEYLLPVWRNDEETPREVGIRYQ 240
D 222 TRGKCYTFNSGDDGRPRLTMTKGTGNGLEIMLDIOQDEYLPVWGTDSTFEAGIKYQ 261
QY 241 IHSQEEPPITDOLGLGVSPGYOTFVSCQOQOQLFLPRPMWDCSSASLNPVYEEPPSPLG 300
D 282 IHSQDEPPITDOLGLGVAPGFQTFVSCQEQRLLYLPSPWGTCAVYWDSDP----- 332
QY 301 SPSPSPSPPTTLMGCRACETRYVARKCGRMVYMGDVVCSPOOYKNCAPHAIDAIR 360
D 333 -----FDSYSTACRIDCTETRYLVENCNCRMYHMPGDAPYCTPEOYKECADPALDFVE 386
QY 361 KDS--CACPNPCASTRAKELSWRIPSRARARLAKRLRSBAYIAENVLADIFEAL 418
D 387 KDQECVCEMPCNLTGRKELSMVKIPSKASAKYLAKEFKSEQYIGENILVLDIFEVL 446
QY 419 NYETVQKRAYESELGLDGGOMGLFICASLITILEILDYLCVFRDKYLGYFMNRQHS 478
D 447 NYETIEQKRAYETAGLGLDGGOMGLFICASLITILELFDYAEVYIKHRLC---RRGKC 502
QY 479 QRHSSTNLQEGLSHRTQVPHLSLGRPPTPPC 512
D 503 QKEAKRSSADKGYA-----LSLDVKKRHNP 528

RESULT 10
ID 055163 PRELIMINARY; PRT; 563 AA.
AC 055163;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE PROTON-GATED CATION CHANNELS MODULATOR SUBUNIT MDEG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037807; PubMed=9368048;
RL Lingueglia E., Demellie E., Bassilana F., Heurteaux C., Sakai H.,

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RA Waldmann R., Lazdunski M.;  
RT "A modulatory subunit of acid sensing ion channels in brain and dorsal  
RT root ganglion cells.";  
RL J. Biol. Chem. 272:29778-29783(1997).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS  
CC FAMILY.  
DR EMBL: Y14635; CAA74979.1; -.  
DR InterPro: IPR001873; ASC.  
DR Pfam: PF00858; ASC. 1.  
DR PROSITE: PS01206; ASC. 1.  
KW Glycoprotein; Ion transport; Ionic channel; Transmembrane.  
SQ SEQUENCE 563 AA: 63115 MW; DCE1BA0A45F21E2 CRC64;  
  
Query Match 43.8%; Score 1249.5; DB 11; Length 563;  
Best Local Similarity 47.5%; Pred. No. 4.5e-106;  
Matches 245; Conservative 79; Mismatches 151; Indels 41; Gaps 8;  
  
OY 6 GPEEAR-OPSDIRVFASNCMHGLGHV---FGPGSLSLRGMAAAVVLVSATFLYOV 60  
DB 50 GPGVARRGRPS-----LSRTKLHGLRHMCAGRTAAGSGFORRALVWLAFCTSLGLLSMS 104  
OY 61 AERVYTYREFHQTLADERESHRLVFPVATLCNINPLRSRLTPNDLMAGSALLGLDPA 120  
DB 105 SNRLLYWLSPSHTRVHREWSKQLPFPVATVCNNPDLRPPRLSKDLYYAGHWGLLPLN 164  
OY 121 EHA-AFLRALGRPPAPG-----FMSPPTFD--MAQLYRAGHSLDMLDCRF 166  
DB 165 RTARPLVSELRLGDEPRRQWFKLADFLRLPFRHFEBSAFAFMRLGHOLEDMLSKCY 224  
OY 167 RGQPGPENFTTIFTRMGKCYTFNSGADGAEILLTTTGGMGNGLDIMLDVQOEEYLPWR 226  
DB 225 RGEIGPNNHFSVFYKCYGKCYFNSGDEGKPLLTIVKGGTGNGLEIMLDIOODEYLPWG 284  
OY 227 DNEETPFEVGIRVOYHSOEPPIIDOLGLGVSFGYQTFVSCQOQLSFLPPMGCCSSAS 286  
DB 285 ETEETTFEAGVAVOYHSOEPPIIDOLGLGVSFGYQTFVSCQOQLSFLPPMGCCSSAS 344  
OY 287 LNPNEPEPSDPLGSPSPSPRYTLMGCRACETRYVYARCKGCRMYVPGDVPCSPQO 346  
DB 345 MGLDF-----FPVYSITACRIDCETRYIVENCNCNMVHPGDAPCTPEQ 389  
OY 347 YKNCNHPAIDALRKDS--CACPNPCASTRYAKELSMVRIPIRRAARLAKLNSEAYI 404  
DB 390 HKECAEPALGLAEKDSNYCLRTPCNLTIRYKELSMVKIPSKTSAKLEKFNSEKI 449  
OY 405 AENVNALDIFFEALNYETVEOKKAYEMSELGDIGOGMLFGASLITLLETIDYLCVF 464  
DB 450 SENILYLDIFFEALNYETVEOKKAYEVALADIGOGMLFGASLITLLETIDYLYELI 509  
OY 465 RDKVLGYFWNRHOSQHSSTNLDEGLSHRTQVPH 500  
DB 510 KEKLLDLGKEEBSGHDENMSTCDTMNHSSETISH 545  
  
RESULT 11  
O61203 PRELIMINARY; PRT; 563 AA.  
AC O61203;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE PROTON-GATED CATION CHANNELS MODULATORY SUBUNIT MEG2 (AMILORIDE-  
DE SENSITIVE CATION CHANNEL 1, NEURONAL) (SODIUM CHANNEL 1).  
GN ACCN1 OR MBNAC1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=BRAIN;  
RX MEDLINE=98037807; PubMed=9368048;

RA Lingueglia E., Demaille E., Bassilana F., Heurteaux C., Sakai H.,  
RA Waldmann R., Lazdunski M.;  
RT "A modulatory subunit of acid sensing ion channels in brain and dorsal  
RT root ganglion cells.";  
RL J. Biol. Chem. 272:29778-29783(1997).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS  
CC FAMILY.  
DR EMBL: Y14634; CAA74978.1; -.  
DR EMBL: U57353; AAB49183.1; -.  
DR MGD: MGI:1100867; Accn1.  
DR InterPro: IPR001873; ASC.  
DR Pfam: PF00858; ASC. 1.  
DR PRINTS: PR01078; AMINACHANNEL.  
DR PROSITE: PS01206; ASC. 1.  
KW Glycoprotein; Ion transport; Ionic channel; Transmembrane.  
SQ SEQUENCE 563 AA: 63204 MW; 56F7BA0A214BA39 CRC64;  
  
Query Match 43.8%; Score 1247.5; DB 11; Length 563;  
Best Local Similarity 47.3%; Pred. No. 6.8e-106;  
Matches 244; Conservative 80; Mismatches 151; Indels 41; Gaps 8;  
  
OY 6 GPEEAR-OPSDIRVFASNCMHGLGHV---FGPGSLSLRGMAAAVVLVSATFLYOV 60  
DB 50 GPGVARRGRPS-----LSRTKLHGLRHMCAGRTAAGSGFORRALVWLAFCTSLGLLSMS 104  
OY 61 AERVYTYREFHQTLADERESHRLVFPVATLCNINPLRSRLTPNDLMAGSALLGLDPA 120  
DB 105 SNRLLYWLSPSHTRVHREWSKQLPFPVATVCNNPDLRPPRLSKDLYYAGHWGLLPLN 164  
OY 121 EHA-AFLRALGRPPAPG-----FMSPPTFD--MAQLYRAGHSLDMLDCRF 166  
DB 165 RTARPLVSELRLGDEPRRQWFKLADFLRLPFRHFEBSAFAFMRLGHOLEDMLSKCY 224  
OY 167 RGQPGPENFTTIFTRMGKCYTFNSGADGAEILLTTTGGMGNGLDIMLDVQOEEYLPWR 226  
DB 225 RGEIGPNNHFSVFYKCYGKCYFNSGDEGKPLLTIVKGGTGNGLEIMLDIOODEYLPWG 284  
OY 227 DNEETPFEVGIRVOYHSOEPPIIDOLGLGVSFGYQTFVSCQOQLSFLPPMGCCSSAS 286  
DB 285 ETEETTFEAGVAVOYHSOEPPIIDOLGLGVSFGYQTFVSCQOQLSFLPPMGCCSSAS 344  
OY 287 LNPNEPEPSDPLGSPSPSPRYTLMGCRACETRYVYARCKGCRMYVPGDVPCSPQO 346  
DB 345 MGLDF-----FPVYSITACRIDCETRYIVENCNCNMVHPGDAPCTPEQ 389  
OY 347 YKNCNHPAIDALRKDS--CACPNPCASTRYAKELSMVRIPIRRAARLAKLNSEAYI 404  
DB 390 HKECAEPALGLAEKDSNYCLRTPCNLTIRYKELSMVKIPSKTSAKLEKFNSEKI 449  
OY 405 AENVNALDIFFEALNYETVEOKKAYEMSELGDIGOGMLFGASLITLLETIDYLCVF 464  
DB 450 SENILYLDIFFEALNYETVEOKKAYEVALADIGOGMLFGASLITLLETIDYLYELI 509  
OY 465 RDKVLGYFWNRHOSQHSSTNLDEGLSHRTQVPH 500  
DB 510 KEKLLDLGKEEBSGHDENMSTCDTMNHSSETISH 545  
  
RESULT 12  
O9NOA4 PRELIMINARY; PRT; 539 AA.  
ID O9NOA4;  
AC O9NOA4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)



DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
DE PUTATIVE ACID-SENSING ION CHANNEL (ACID SENSING ION CHANNEL 4).  
GN ASIC4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=PUTATIVE;  
RX MEDLINE=20309050; PubMed=10852210;  
RA Grunler S., Geisler H.S., Baessler E.L., Ruppersberg J.P.;  
RT "A new member of acid-sensing ion channels from pituitary gland.";  
RN Neuroreport 11:1607-1611(2000).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2145362; PubMed=1571555;  
RA Grunler S., Geisler H.S., Rainier S., Fink J.K.;  
RT "Acid-sensing ion channel (ASIC) 4 gene: physical mapping, genomic  
RT organisation, and evaluation as a candidate for paroxysmal dystonia.";  
RL Eur. J. Hum. Genet. 9:672-676(2001).  
DR EMBL: AJ271643; CAB93980.1; -  
DR EMBL: AJ408881; CAC51338.1; -  
DR EMBL: AJ408882; CAC51338.1; JOINED.  
DR EMBL: AJ408883; CAC51338.1; JOINED.  
DR EMBL: AJ408884; CAC51338.1; JOINED.  
DR Interpro: IPR001873; ASC.  
DR Pfam: PF00858; ASC; 2.  
DR PRINTS: PRO1078; AMINACHANNEL.  
SQ SEQUENCE 539 AA; 59206 MW; 9C7ACF0DF5EC17E9 CRC64;

Query Match 41.4%; Score 1180; DB 4; Length 539;  
Best Local Similarity 49.8%; Pred. No. 1e-99;  
Matches 247; Conservative 58; Mismatches 161; Indels 30; Gaps 9;

QY 14 PSIRVAFASMSMGHGVPGSLSRGMAAAVLSVATFLYQVAERVRYREHHQ 73  
DB 39 PRDAIFASTSTLHGACGPGHGRRLMALTLTSLAFLYQVAGLAGLTPH 98  
QY 74 TALDERSHLV-FPAVTLNINPLRSLRTPNDL-HWAGSALLGLDPAEHAFLRALGR 131  
DB 99 VANDPAPAPVAGPRAVATLCLNINFRHSALSDADIFHLAN--LTGLPRKDRDGRAGLR 156  
QY 132 PPAAPGFPSPPTDMAOLYARAGSHLDDMLDCFRGQPCGPNFTTIFTRMKCYTENS 191  
DB 157 YPEP-----DMDILNRGTHQDLADMLKSCNFGHSCASNFVYTRYGKCTFN- 206  
QY 192 GAGCAELLTTTRGGMGNDLMDVQOEYLPWRDNEFPFEVGIIVQIHSHOEPPIID 251  
DB 207 -ADPRSSLPFRAGMGSLIMLDIOOEYLPWRDNEFPFEVGIIVQIHSHOEPPIID 265  
QY 252 QLGAGVSPGYOTFVSCQOOLSFLLPPMGDCSSASLNPNTEPEPSDPLGSPSPSPYT 311  
DB 266 QLGAGVSPGYOTFVSCQOOLSFLLPPMGDCSSASLNPNTEPEPSDPLGSPSPSPYT 311  
QY 312 LMGRCLACETRYVARKCGCRMYVPGDVPVCSPOQYKNCAPDAIDAI--LRKSCACPNP 369  
DB 315 VSACRLCEKEAVLQORCHRMVMPNETICPNPIYIECADHTLDSGGEGEGFCPTP 374  
QY 370 CASRRAKESIMVIRPSRAARFLARKINSEAVIAENVLALDIFFEALNTEYEOKKAY 429  
DB 375 CNLIRKELISWRIIPKRSARYLARKYNNREYIIRNFVLVDVFEALNSEAEOORAY 434  
QY 430 EMBELDGGOMGLFAGSLTFLLEILDYLCVFRDKVLGYEWNROSHSSTNLLOE 489  
DB 435 GLSALLDGGOMGLFAGSLTFLLEILDYLYEVSWDR-LKRVARRKPTPLRTSTGIST 493  
QY 490 -GLGSHRTQVPHSLG 504  
DB 494 LGLDELKEQSPSLG 509

RESULT 13  
QYHS6 ID QYHS6 PRELIMINARY; PRT; 539 AA.  
AC QYHS6;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE PUTATIVE ACID-SENSING ION CHANNEL.  
GN ASIC4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRNIN;  
RX MEDLINE=20309050; PubMed=10852210;  
RA Grunler S., Geisler H.S., Baessler E.L., Ruppersberg J.P.;  
RT "A new member of acid-sensing ion channels from pituitary gland.";  
RN Neuroreport 11:1607-1611(2000).  
DR EMBL: AJ271642; CAB93984.1; -  
DR Interpro: IPR001873; ASC.  
DR Pfam: PF00858; ASC; 2.  
DR PRINTS: PRO1078; AMINACHANNEL.  
SQ SEQUENCE 539 AA; 59324 MW; 3D73DE0EAEFF7097 CRC64;

Query Match 41.0%; Score 1169; DB 11; Length 539;  
Best Local Similarity 48.7%; Pred. No. 1e-98;  
Matches 243; Conservative 60; Mismatches 166; Indels 30; Gaps 9;

QY 6 GREARQPSDIRVAFASMSMGHGVPGSLSRGMAAAVLSVATFLYQVAERVR 65  
DB 31 GAAGPAPRDLATFASTSTLHGACGPGHGRRLMALTLTSLAFLYQVAGLAGLTPH 90  
QY 66 YRFEHHQTALEDERSHLV-FPAVTLNINPLRSLRTPNDL-HWAGSALLGLDPAEHA 123  
DB 91 CYLIRPHLVANDPAPAPVAGPRAVATLCLNINFRHSALSDADIFHLAN--LTGLPRKDRD 148  
QY 124 AFLRALGRPAPGFPSPPTDMAOLYARAGSHLDDMLDCFRGQPCGPNFTTIFTRMK 183  
DB 149 GHRAAGLRPEP-----DMDILNRGTHQDLADMLKSCNFGHSCASNFVYTRY 199  
QY 184 GKCTFNSGADGALLTTTRGGMGNDLMDVQOEYLPWRDNEFPFEVGIIVQIHSHO 243  
DB 200 GKCTFEN--ADPOSSLPRAGMGSLIMLDIOOEYLPWRDNEFPFEVGIIVQIHSHO 257  
QY 244 QEEPPPIIDLGAGVSPGYOTFVSCQOOLSFLLPPMGDCSSASLNPNTEPEPSDPLGSPS 303  
DB 258 QEEPPPIIDLGAGVSPGYOTFVSCQOOLSFLLPPMGDCSSASLNPNTEPEPSDPLGSPS 303  
QY 304 PPSPPYTLMGCRCLACETRYVARKCGCRMYVPGDVPVCSPOQYKNCAPDAIDAI--LRK 361  
DB 307 LOGSAYSVSACRLCEKEAVLQORCHRMVMPNETICPNPIYIECADHTLDSGGEGSE 366  
QY 362 DSCACPNPCASTRYAKELISWRIIPKRSARYLARKYNNREYIIRNFVLVDVFEALNSE 421  
DB 367 GPCCFPTPCNLIRKELISWRIIPKRSARYLARKYNNREYIIRNFVLVDVFEALNSE 426  
QY 422 TVEOKKAYEMSELGIDGGOMGLFAGSLTFLLEILDYLCVFRDKVLGYEWNROSHS 481  
DB 427 AMEORAYGLSALLDGGOMGLFAGSLTFLLEILDYLYEVSWDR-LKRVARRKPTPLR 485  
QY 482 SSTNLLOE-GLGSHRTQV 499  
DB 486 TSTGISTLGLDELKEQSP 504

RESULT 14  
QYHS6 ID QYHS6 PRELIMINARY; PRT; 539 AA.  
AC QYHS6;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)

01-JUN-2001 (Tremblrel. 17, last annotation update)  
DE SPASIC PROTEIN.  
GN SPASIC.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_Taxid=10116;  
RN  
[1]  
SEQUENCE FROM N.A.  
RA Akopian A.N., England S., Chen C.C., Wood J.N.;  
RT "A non-inactivating proton-gated ion channel is broadly expressed in  
the central nervous system."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ242534; CAB61836.1; -.  
DR InterPro; IPR001873; ASC.  
DR Pfam; PF00858; ASC; 2.  
DR PRINTS; PRO1078; AMINACHANNEL.  
SQ SEQUENCE 539 AA; 59352 MW; 2DE4838AA0547097 CRC64;

Query Match 40.9%; Score 1167; DB 11; Length 539;  
Best Local Similarity 48.5%; Pred. No. 1.6e-98;  
Matches 242; Conservative 61; Mismatches 166; Indels 30; Gaps 9;

QY 6 GEEARQPSDTRVFNASHGNGHVGPGSLSRGGMMAAVVSVATFLYQVAERVR 65  
DB 31 GAAQPPARPRLATFASSTLHGLGRACGPGHGLRTLMVLAFLTSLAFLYQAASLAR 90  
QY 66 YRREFHQTALDERSHRLV-FPAVTLNINPLRRSLTPNDL-HWAGSALLGDPAEHA 123  
DB 91 GYLTRPHLVAMPDAPAPVAGFPATVLCNINFRHSALSDADIFILAN--LTGLPRKQND 148  
QY 124 AFLRLGRRPAPPGFMPSTFDMALYARAGHSLDMLDCRFKQPCGPFENFTITFRM 183  
DB 149 GHRAAGLRYPEP-----DMVDILNRTGHQLADMLKSCNFSGHCSASNSFVYTRY 199  
QY 184 GKCYFNSGADAEALLTTTGGMGNGLDMLDVOOEYLPVRDNEETPREVGIVQHS 243  
DB 200 GKCYTFN--ADQSSLPFRAGMGSGLEMLDIOEEYLPVIMETNETSEAGIRVQHS 257  
QY 244 QEEPIIDOLGVSFGYQTEVSCQOOLSFLLPPMGDCSSASLNPYEPSPSPSPYT 303  
DB 258 QEEPIYIHLGFGVSPGOTFVSCQOOLRLLYLPQPMGNCRAES-----KLREPE 306  
QY 304 PPSPPYTLMGCRCLACETRYVARKCGCRMYVPGDVPVCSPOQYKNCAPDAIDAI--LRK 361  
DB 307 LOGYSAYSVSACRLCEKAEVLRCHCRMYHMPGNETTICPPNITECADHTLDSLGSE 366  
QY 362 DSCACPNPCASTRYAKESLNVIPRRAARFLARKLNSEAVIAENVLALDIFFEALNVE 421  
DB 367 GPCFPTCNLTRYKEISMKVTPRGSARKYLARKYNNRETYIRENPLVDVFEALTISE 426  
QY 422 TVEOKKAYEMSELDDIGOMGLFTGASLLTLEILDYLCYEFVRDKVLGYFNRRHQSQRH 481  
DB 427 AMEQRAAYGLSALLGDLGOMGLFTGASLLTLEILDYIYEVSMWR-LKRVRRRKTPLR 485  
QY 482 SSTNLDE-GLGSHTQVP 499  
DB 486 TSTGISTLGLQELKEQSP 504

RESULT 15

096FT7 PRELIMINARY; PRT; 647 AA.  
AC 096FT7;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:17248).  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_Taxid=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010439; AAH10439.1; -.  
SQ SEQUENCE 647 AA; 70033 MW; 87333716882872D0 CRC64;

Query Match 39.7%; Score 1130.5; DB 4; Length 647;  
Best Local Similarity 48.7%; Pred. No. 4.7e-95;  
Matches 242; Conservative 53; Mismatches 151; Indels 51; Gaps 10;

QY 14 PEDIIVFASNCMGHGLHVGPGSLSRGGMMAAVVSVATFLYQVAERVRYYEFTHQ 73  
DB 166 PDLATFASSTLHGLGRACGPGHGLRTLMVLAFLTSLAFLYQAAGLGYLTRPHL 225  
QY 74 TALDERSHRLV-FPAVTLNINPLRRSLTPNDL-HWAGSALLGDPAEHAFLALGR 131  
DB 226 VAMDPAAPAPVAGFPATVLCNINFRHSALSDADIFILAN--LTGLPRKDRGHNAAGLR 283  
QY 132 PPAPGFMPSPTFDMALYARAGHSLDMLDCRFKQPCGPFENFTITFRMGKCYTENS 191  
DB 284 YPEP-----DMVDILNRTGHQLADMLKSCNFSGHCSASNSFVYTRYGKCYTFN- 333  
QY 192 GADGAEALLTTTGGMGNGLDMLDVOOEYLPVRDNEETPREVGIRVQHSQEEPIID 251  
DB 334 -ADPSSSLPFRAGMGSGLEMLDIOEEYLPVIMETNETSEAGIRVQHSQEEPIYH 392  
QY 252 QGLGVSPGYQTEVSCQOOLSFLLPPMGDCSSASLNPYEPSPSPSPYT 311  
DB 393 QUGFVSGFOTFVSCQOOLRLLYLPQPMGNCRAES-----ELREPELGYSAYS 441  
QY 312 IMGCRCLACETRYVARKCGCRMYVNP--GDVPVCSPOQYKNCAPDAIDAILRKDSCACP 368  
DB 442 VSACRLRCEKAEVLRCHCRMYHMPDLSLGGP-----EGPCFPT 481  
QY 369 PCASTRYAKESLNVIPRRAARFLARKLNSEAVIAENVLALDIFFEALNVEYEQKA 428  
DB 482 PCNLTTRYKEISMKVTPRGSARKYLARKYNNRETYIRENPLVDVFEALTISEAENQRAA 541  
QY 429 YEMSELDDIGOMGLFTGASLLTLEILDYLCYEFVRDKVLGYFNRRHQSQRHSTNLQ 488  
DB 542 YGLSALLDGLGOMGLFTGASLLTLEILDYIYEVSMWR-LKRVRRRKTPLRSTGIS 600  
QY 489 E-GLGSHTQVPNLSLG 504  
DB 601 TLGLQELKEQSPSLG 617

Search completed: October 11, 2002, 07:26:20  
Job time : 93 secs

Fri Oct 11 09:49:28 2002

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 11, 2002, 03:46:04 : Search time 65 seconds  
(without alignments)  
907.387 Million cell updates/sec

Title: US-09-530-233-2  
Perfect score: 2851  
Sequence: 1 MKPTSGPEARQPSDIRVF.....CAVTKTLASHTCYLVTQL

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
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- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
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- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2851	100.0	531	20	AA09509
2	2833	99.4	531	21	AA09181
3	2706	94.9	549	20	AAW8252
4	2598	91.1	543	20	AAW8250
5	2481	87.0	518	20	AAW8251
6	2447	85.8	533	19	AAW8508
7	2447	85.8	533	21	AAW69179
8	1365	47.9	512	19	AAW68506
9	1365	47.9	512	20	AAW93420
10	1365	47.9	512	21	AAW69177
11	1340	47.0	513	20	AAV03186

ALIGNMENTS

12	1337	46.9	559	19	AAW68507	Rat acid sensing 1
13	1337	46.9	559	21	AAW69178	A rat acid-sensitl
14	1329	46.6	526	19	AAW68504	Rat acid sensing 1
15	1329	46.6	526	20	AAV03188	Rat Acid sensitive
16	1329	46.6	526	21	AAW69175	A rat acid-sensitl
17	1319	46.3	514	19	AAW68505	Human acid sensing
18	1319	46.3	514	21	AAW69176	A partial acid-sen
19	1249.5	43.8	563	19	AAW68509	Rat acid sensing 1
20	1246.5	43.7	563	21	AAW69180	A rat acid-sensitl
21	1180	41.4	539	19	AAW80318	Neurodegenerative
22	1180	41.4	539	22	AAE10897	Human brain sodium
23	1175	41.2	539	19	AAW80315	Neurodegenerative
24	1174	41.2	539	22	AAE10898	Human brain sodium
25	1170	41.0	539	21	AAV53870	Amino acid sequenc
26	1134.5	39.8	587	19	AAW80316	Neurodegenerative
27	806.5	28.3	401	21	AAW807750	A human acid sensi
28	616	21.6	505	22	AAW91115	Amino acid sequenc
29	614	21.5	505	22	AAW91118	Amino acid sequenc
30	613	21.5	505	22	AAW91116	Amino acid sequenc
31	613	21.5	505	22	AAW91117	Amino acid sequenc
32	532.5	18.7	707	20	AAV03187	Novel human diagno
33	369.5	13.0	493	13	AAW24674	Mec-4 gene product
34	342.5	12.0	493	13	AAW20107	Mec-4 gene product
35	342.5	12.0	493	14	AAW33890	mec-4 protein. Ca
36	335.5	11.8	150	22	AAW16915	Human nervous syst
37	335.5	11.8	150	22	AAW42375	Human polypeptide
38	328	11.5	103	19	AAW80317	Neurodegenerative
39	326	11.4	508	14	AAW42747	deg-3 gene product
40	315.5	11.1	669	22	AAE10335	Human transporter
41	298.5	10.5	562	14	AAW42743	mec-4 gene product
42	254	8.9	294	13	AAW20106	deg-1 gene product
43	254	8.9	294	14	AAW33889	deg-1 protein. Ca
44	248.5	8.7	548	22	ABW58115	Drosophila melanog
45	247.5	8.7	516	22	ABW53689	Drosophila melanog

RESULT 1  
AA09509 standard; Protein: 531 AA.

AA09509; 16-JUL-1999 (first entry)

Human proton-gated cation channel.

Human: non-inactivating aniloride-sensitive proton-gated cation channel;

hASIC3; analgesic.

Homo sapiens.

MO9921981-AL

06-MAY-1999.

29-OCT-1998; 98WO-CA01016.

29-OCT-1997; 97CA-2219713.

(UYMC-) UNIV MCGILL.  
Babinski K, Seguela P.  
WPI: 1999-312958/26.  
N-PSDB: AAX56237.  
Use of human protein as a proton-gated cation channel  
Claim 1; Fig 1; 32pp; English.



XX	29-MAR-1999	(first entry)
DT		
XX	Sodium channel receptor hSLINAC1 splice variant.	
DE		
XX	hSLINAC1; sodium channel receptor; human; algesia; analgesia.	
KW		
XX	Homo sapiens.	
OS		
XX	WP09854316-A1	X histone 120
PN		
XX	03-DEC-1998.	
PD		
XX	15-MAY-1998;	possible
PF	98WO-EP02884.	resequence
PR	30-MAY-1997;	
XX	97EP-0401196.	
XX	(SYNO ) SYNTHELABO.	
PA		
XX	Besnard F, Graham D, Renard S;	
PI		
DR	WPI; 1999-070215/06.	
N-PSDB;	AAV84191.	
XX		
PT	A new sodium channel receptor - useful for, e.g. treatment of	
PT	neuronal degenerate problems, Alzheimer's, Parkinson's disease and	
PT	morphine dependence	
XX		
PS	Claim 28; Page 47-49; 63pp; English.	
XX		
CC	This is the amino acid sequence of a splice variant of a new human	
CC	sodium channel receptor (see AAV8250), termed hSLINAC1. It is	
CC	encoded by a polynucleotide (see AAV84191) that was obtained from	
CC	dorsal root ganglia cDNA by PCR amplification using primers (see	
CC	V842120-21) based on the hSLINAC1 polynucleotide (see AAV84189).	
CC	hSLINAC1 is a member of a new class of sodium channel proteins that	
CC	may be responsible for some nervous system transmissions, or may be	
CC	used as a target to regulate some transmissions linked to various	
CC	pathologies. The splice variant cDNA has a 79-nucleotide insert in	
CC	the 3' portion of the coding region. This alters the reading	
CC	frame. As dorsal root ganglia are involved in pain perception, the	
CC	splice variant protein is expected to have a function linked to	
CC	algesia or analgesia.	
XX		
SQ	Sequence 549 AA;	
	Query Match	94.9%; Score 2706; DB 20; Length 549;
	Best Local Similarity	93.9%; Pred. No. 6.8e-241;
	Matches 511; Conservative	3; Mismatches 14; Indels 16; Gaps 2;
QY	1 MKPTSGPEEARROPDSIDIRVFASNCSMHGIGHFVGCSLSLRGMMAAAVVLVSATPFLYOY	60
Dd	1 MKPTSGPEEARPPADIVFAFASNCMHGIGHFVGCSLSLRGMMAAAVVLVSATPFLYOY	60
QY	61 AERVRYVEFHQTALDERESHRLVFPVATTCINIPLRRSRLTPNDLHWAGSALLGLDPA	120
Dd	61 AERVRYVEFHQTALDERESHRLIFPAVTLCINIPLRRSRLTPNDLHWAGSALLGLDPA	120
QY	121 EHAALRLALGRPPAPPGMPSPTEPMALQLYAAGHSIDMLDCRGGPCGPENNTTTF	180
Dd	121 EHAALRLALGRPPAPPGMPSPTEPMALQLYAAGHSIDMLDCRGGPCGPENNTTTF	180
QY	181 TRMGKCYFNFGSADAEILLTTTRGCMGNGLDLMVDQOEYLVPVRDNERTFEVGIHQ	240
Dd	181 TRMGKCYFNFGSADAEILLTTTRGCMGNGLDLMVDQOEYLVPVRDNERTFEVGIHQ	240
QY	241 IHSQEPLITDLGLGVSPGYOTFYSCQQOOLSTLPPEMDCSSASLANPYEPESDPLG	300
Dd	241 IHSQEPLITDLGLGVSPGYOTFYSCQQOOLSTLPPEMDCSSASLANPYEPESDPLG	300
QY	301 SPSPSPSPPYTLTGCRILCETRYVARKGCCRMVWMDPVVCSPOQYKKCAHPATDAIIR	360
Dd	301 SPSPSPSPPYTLTGCRILCETRYVARKGCCRMVWMDPVVCSPOQYKKCAHPATDAIIR	360

OY 361 KDSQCPNCASTRAKELSWRIPSPRAAEFLARKNRSAPYAENVALLDFFELANT 420  
 DB 361 KDSQCPNCASTRAKELSWRIPSPRAAEFLARKNRSAPYAENVALLDFFELANT 420  
 OY 421 ETVEQKAYEAKSELLGDIGGOMGEFIGASLLTLEILDYLCVEFRDXVIGYFMNRHOSQR 480  
 DB 421 ETVEQKAYEAKSELLGDIGGOMGEFIGASLLTLEILDYLCVEFRDXVIGYFMNRHOSQR 480  
 OY 481 HSTNTLLOBEGLSHRTQVPHSLSPR-----PP-----TPPCAVTKTILSASHRT 524  
 DB 481 HSTNTLLOBEGLSHRTQVPHSLSPR-----PP-----TPPCAVTKTILSASHRT 524  
 OY 525 CYLV 528  
 DB 541 AVCV 544  
 RESULT 4  
 AANW88250  
 ID AANW88250 standard; Protein: 543 AA.  
 XX AANW88250;  
 DT 29-MAR-1999 (first entry)  
 XX Sodium channel receptor hSLINACL.  
 DE hSLINACL; sodium channel receptor; human; neurodegeneration;  
 KM Alzheimer's disease; Parkinson's disease; morphine dependence;  
 KM chorea; muscular spasm; epilepsy; stroke; cardiac disease;  
 KM schizophrenia; depression; nicotine dependence;  
 KM amyotrophic lateral sclerosis; multiple sclerosis; inflammation;  
 KM pain; cancer; obesity; neurotransmitter; analgesic; anaesthesia.  
 XX Homo sapiens.  
 OS  
 XX  
 PN MW0854316-AI.  
 XX 03-DEC-1998.  
 PD  
 XX 15-MAY-1998; 98WO-EP02884.  
 PF  
 XX 30-MAY-1997; 97EP-040116.  
 PR  
 XX (STNO ) SINTHELABO.  
 PA  
 XX Besnard F, Graham D, Renard S;  
 PI WPI: 1999-070215/06.  
 DR N-PSDB: AANW84189.  
 XX  
 PT A new sodium channel receptor - useful for, e.g. treatment of  
 PT neuronal degenerate problems, Alzheimer's, Parkinson's disease and  
 PT morphine dependence  
 Claim 1; Page 35-36; 63pp; English.  
 This is the amino acid sequence of a new human sodium channel  
 receptor, termed hSLINACL, as deduced from an isolated cDNA clone  
 (see AANW84189). hSLINACL is a member of a new class of sodium channel  
 proteins that may be responsible for some nervous system  
 transmissions, or may be used as a target to regulate some  
 transmissions linked to various pathologies. Methods for producing  
 hSLINACL polypeptides by recombinant methods are disclosed. Host  
 cells expressing hSLINACL can be used to screen for agonists or  
 antagonists of hSLINACL. Such compounds can be used to treat  
 neurodegeneration, hyperalgesia, Alzheimer's disease, Parkinson's  
 disease, chorea, muscular spasm, epilepsy, stroke, cardiac disease,  
 schizophrenia, depression, nicotine dependence, morphine dependence,  
 amyotrophic lateral sclerosis, multiple sclerosis, inflammation,  
 pain, cancer and obesity, to mimic or antagonise the effects of  
 endogenous transmitter peptides/opioids or anti-opioids, to alter

CC gustative perception, to cause analgesia or anaesthesia, or to  
CC diagnose or treat any disorder related to abnormal expression of  
CC hSLNAC1.  
XX  
SQ Sequence 543 AA;

Query Match 91.1%; Score 2598; DB 20; Length 543;  
Best Local Similarity 93.9%; Pred. No. 6.2e-231;  
Matches 491; Conservative 4; Mismatches 12; Indels 16; Gaps 3;

QY 1 MKPTSGPEARPPSDIVFASNCMHGIVFGSGISLRGMMAAVVLSVATFLYQV 60  
DB 1 MKPTSGPEARPPSDIVFASNCMHGIVFGSGISLRGMMAAVVLSVATFLYQV 60  
QY 61 AERVYREFHQTALDERESHRLVFPVATLCINIPLRSLTPNDLHMAGSALLGLDPA 120  
DB 61 AERVYREFHQTALDERESHRLVFPVATLCINIPLRSLTPNDLHMAGSALLGLDPA 120  
QY 121 EHAFLRALGRPPAPPGFMPSPFTFDMQLYARAGSLDMLDCRFRCQPCPENFTTIF 180  
DB 121 EHAFLRALGRPPAPPGFMPSPFTFDMQLYARAGSLDMLDCRFRCQPCPENFTTIF 180  
QY 181 TRMGCTYFNSGADGAEELTTTRGGMNGLDIMLDVQOEYLPVNRDNEETPFEVGIRVQ 240  
DB 181 TRMGCTYFNSGADGAEELTTTRGGMNGLDIMLDVQOEYLPVNRDNEETPFEVGIRVQ 240  
QY 241 IHSQEEPIIDQLGLGVSFGYQTEFVSCQOQSLFPLPPMGDCSSASLNPTEPEPSDPLG 300  
DB 241 IHSQEEPIIDQLGLGVSFGYQTEFVSCQOQSLFPLPPMGDCSSASLNPTEPEPSDPLG 300  
QY 301 SPSPSPSPPYTLMLGCRCLACETRIVYARCKGCRMYMPGDVPCSPQOYKNCAPALDAILR 360  
DB 301 SPSPSPSPPYTLMLGCRCLACETRIVYARCKGCRMYMPGDVPCSPQOYKNCAPALDAILR 360  
QY 361 KDSQCPKPCASTRAKELSVRIIPSRRAARFLARKLNRESEYIAENVALDIDFEALNY 420  
DB 361 KDSQCPKPCASTRAKELSVRIIPSRRAARFLARKLNRESEYIAENVALDIDFEALNY 420  
QY 421 ETVQKKAEMSESLDIDGOMGLFYGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSOR 480  
DB 421 ETVQKKAEMSESLDIDGOMGLFYGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSOR 480  
QY 481 HSTINLQOE-GLGSHRTQV---PHL-----SLGPRP 507  
DB 481 HSTINLQOE-GLGSHRTQV---PHL-----SLGPRP 507

RESULT 5  
AAW88251  
ID AAW88251 standard; Protein: 518 AA.

XX AC AAW88251;  
XX DT 29-MAR-1999 (first entry)  
XX DE Sodium channel receptor hSLNAC1 homologous polypeptide.  
XX KM hSLNAC1; sodium channel receptor; human.  
XX OS Homo sapiens.

AAW88251  
BN W09854366-A1  
PB 03-DEC-1998

PF 15-MAY-1998; 98MO-EP02884.  
XX 30-MAY-1997; 97PF-0401196.  
XX (SYNO) SYNTHETIC  
XX PA (SYNO) SYNTHETIC  
XX PI Renard F, Graham D, Renard S;  
XX

*possible interaction  
with protein 518*

DR WPI: 1999-070215/06.  
DR N-PSDB: AAW84190.  
XX  
XX A new sodium channel receptor - useful for, e.g. treatment of  
XX neuronal degenerate problems, Alzheimer's, Parkinson's disease and  
XX morphine dependence  
PS Claim 24; Page 41-42; 63pp; English.

This polypeptide shows homology to the novel human sodium channel  
receptor hSLNAC1 (see AAW88251). It is encoded by a cDNA clone (see  
AAW84190) derived from the human cerebellum. hSLNAC1 is a member of  
a new class of sodium channel proteins that may be responsible for  
some nervous system transmissions, or may be used as a target to  
regulate some transmissions linked to various pathologies.  
Agonists and antagonists of hSLNAC1 activity can be used to treat  
e.g. neurodegenerative problems, morphine or nicotine dependency,  
or cancer.

Sequence 518 AA;

Query Match 87.0%; Score 2481; DB 20; Length 518;  
Best Local Similarity 94.0%; Pred. No. 3.7e-220;  
Matches 468; Conservative 4; Mismatches 10; Indels 16; Gaps 3;

QY 26 MHGLHVEGPGSLSLRRGMMAAVVLSVATFLYQVAEVRVRYREFHQTALDERESHRLV 85  
DB 1 MHGLHVEGPGSLSLRRGMMAAVVLSVATFLYQVAEVRVRYREFHQTALDERESHRLV 85  
QY 86 FPVATLCINIPLRSLTPNDLHMAGSALLGLDPAEHAFLRALGRPPAPPGFMPSPFTD 145  
DB 61 FPVATLCINIPLRSLTPNDLHMAGSALLGLDPAEHAFLRALGRPPAPPGFMPSPFTD 120  
QY 146 MAQLYARAGHSLDMLDCRFRCQPCPENFTTIFTRMGCTYFNSGADGAEELTTTRGG 205  
DB 121 MAQLYARAGHSLDMLDCRFRCQPCPENFTTIFTRMGCTYFNSGADGAEELTTTRGG 180  
QY 206 MNGGLDMLDVQOEYLPVNRDNEETPFEVGIRVQIHSQEEPIIDQLGLGVSFGYQTEFV 265  
DB 181 MNGGLDMLDVQOEYLPVNRDNEETPFEVGIRVQIHSQEEPIIDQLGLGVSFGYQTEFV 240  
QY 266 SCQOQOQSLFPLPPMGDCSSASLNPTEPEPSDPLGSPSPPYTLMLGCRCLACETRIVA 325  
DB 241 SCQOQOQSLFPLPPMGDCSSASLNPTEPEPSDPLGSPSPPYTLMLGCRCLACETRIVA 300  
QY 326 RKCCGRMYMPGDVPCSPQOYKNCAPALDAILRKDSCACPNPCASTRAKELSMVRIP 385  
DB 301 RKCCGRMYMPGDVPCSPQOYKNCAPALDAILRKDSCACPNPCASTRAKELSMVRIP 360  
QY 386 SRAARFLARKLNRESEYIAENVALDIDFEALNYETVQKKAEMSESLDIDGOMGLF 445  
DB 361 SRAARFLARKLNRESEYIAENVALDIDFEALNYETVQKKAEMSESLDIDGOMGLF 420  
QY 446 IGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSSTNLTQOE-GLGSHRTQV---PHL 501  
DB 421 IGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSSTNLTQOE-GLGSHRTQV---PHL 480  
QY 502 -----SLGPRP 507  
DB 481 LPCHTALDLVSSSEPRP 498

RESULT 6  
AAW68508  
ID AAW68508 standard; Protein: 533 AA.

XX AC AAW68508;  
XX DT 02-FEB-1999 (first entry)  
XX DE Rat acid sensing ionic channel DRASIC.  
XX KM Rat; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;

KW acid sensing ionic channel; hybridisation: primer: PCR: amplification:  
 KW modulator: acidity: nociception: pain: taste: inflammation: ischaemia;  
 KW tumour: cerebral neurodegeneration: transgenic animal: knockout animal;  
 KW gene therapy: Alzheimer's; Parkinson's; Huntington's; disease;  
 KW amyotrophic lateral sclerosis; cerebellar ataxia.

OS Rattus sp.

PN MO9835034-A1.

XX 13-AUG-1998.

XX 11-FEB-1998;

XX 98MO-PR00270.

XX 28-JUL-1997; 97FR-0009587.

XX 11-FEB-1997; 97FR-0001574.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Basillana F, Champigny G, Heurteaux C, Lazdunski M;

XX Waldegg R, Lingueglia E;

XX WPI; 1998-447231/38.

XX N-PSDB; AAV60843.

XX Protein comprising proton-sensitive neuronal channel - useful for

XX screening for analgesics and for treating neurodegeneration

XX Claim 6; Page 38-40; 64pp; French.

This sequence represents the rat Acid Sensing Ionic Channel (ASIC)  
 CC DRASIC protein, a member of the neuronal cationic channel family that  
 CC are sensitive to amiloride and activated by protons. The DRASIC gene  
 CC is expressed in sensory neuronal cell rather than in the brain as with  
 CC other members of the ASIC gene family. The protein can be used to  
 CC screen for modulators of these channels, particularly to identify  
 CC compounds that modulate perception of acidity, as regards nociception  
 CC (pain) rather than taste. These compounds are used to treat or prevent  
 CC pain associated with acidity (e.g. in cases of inflammation, ischaemia  
 CC or some tumours) and as inhibitors of neurodegeneration caused by  
 CC overexpression of the channels. Antibodies to the protein are used to  
 CC detect the channels in tissues, and to act therapeutically as channel  
 CC modulators. The nucleic acid can be used to generate transgenic,  
 CC particularly knockout, animals for studying ASIC-related disorders,  
 CC also for gene therapy. The channel protein, or its (ant)agonists, can  
 CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.  
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral  
 CC sclerosis or cerebellar ataxia.

SQ Sequence 533 AA;

Query Match

Best Local Similarity 85.8%;

Matches 445; Conservative 49; Mismatches 37; Indels 2; Gaps 2;

Score 2447; DB 19; Length 533;

Pred. No. 5.3e-217;

1 MKPTSGPEEA-RROPDIRFASNCMIGHYFGPSILRGMMAAVLVAVFLVQ 59

1 MKPRSLERQKROASDIRFASCTMIGHYFGPSILRGMMAAVLVAVFLVQ 60

60 VAEVRYEYEFHQTALDERESHRLVPAVTLICNINPLRSRLTPNDLHWGSAALGLDP 119

61 VAEVRYEYEFHQTALDERESHRLVPAVTLICNINPLRSRLTPNDLHWGSAALGLDP 120

120 AEAALALRALGRPARPGPSTFPMALQYARAGSLDMLDCRFRCPCPENVFTT 179

121 AEAALALRALGRPARPGPSTFPMALQYARAGSLDMLDCRYRQPCGPENVFTT 180

180 FTFMGKCYFNAGDAGALLTTRGGMNGDMLDVOOEYLPVWRNDEPFEFGIRV 239

181 FTFMGKCYFNAGDAGALLTTRGGMNGDMLDVOOEYLPVWRNDEPFEFGIRV 240

240 QIHSGEPPILDLGLGVSPGYTFVSCQOQQLSFLPPWGDSSSLNP-NYEPEPSDP 298

DB 241 QIHSGEPPILDLGLGVSPGYTFVSCQOQQLSFLPPWGDSSSLNP-NYEPEPSDP 300

QY 299 LGSPPSPSPPTLTMGCRACETRYARCKGCMYMPEDVPYCSQYKNCAPALDI 358

DB 301 LGSPPSPSPPTLTMGCRACETRYARCKGCMYMPEDVPYCSQYKNCAPALDI 360

QY 359 LKRDSCAPNCPASTRYAKELSMVRIPSRRAARFLARKINRSRATYAEVNLADIFEEAL 418

DB 361 LKRDSCAPNCPASTRYAKELSMVRIPSRRAARFLARKINRSRATYAEVNLADIFEEAL 420

QY 419 NYETVEOKKAYEMSELLDYGOMGLFISALTLTLEIIDYCEVPRDVLGFYNNRHS 478

DB 421 NYETVEOKKAYEMSELLDYGOMGLFISALTLTLEIIDYCEVPRDVLGFYNNRHS 480

QY 479 QHRSSTNLQEGISHRTQVPHSLGPRPPPCAVTKTSLASHRTCYLVTL 531

DB 481 QHRSSTNLQEGISHRTQVPHSLGPRPPPCAVTKTSLASHRTCYLVTL 533

RESULT 7

AA69179

ID AAY69179 standard; Protein; 533 AA.

XX AAY69179;

AC AAY69179;

XX 30-MAY-2000 (first entry)

DE A rat acid-sensitive cationic channel 3 (rASIC3).

XX Neuronal acid-sensitive cation channel; ASIC; ASIC 3;

KW proton-gated cation channel; biphasic desensitisation; amiloride;

XX cation transport channel; acid sensor; pH detection.

OS Rattus sp.

XX WO200008149-A2

XX 17-FEB-2000;

XX 05-AUG-1998; 99WO-IB01445.

XX 05-AUG-1998; 98US-0095408.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Waldmann R, Basillana F, Lazdunski M, De Welle JR;

XX WPI; 2000-195574/17.

XX N-PSDB; AAG61201.

XX Novel human cation transport protein, Acid Sensing Ionic Channel 3 used

XX to identify substances capable of modulating cation transport channel

XX activity

PS Disclosure; Page 77-79; 84pp; English.

XX The present sequence represents a rat neuronal acid-sensitive cation

XX channel 3 (ASIC3) protein. The protein is a proton-gated cation

XX channel subunit that has biphasic desensitisation kinetics with both

XX a rapidly inactivating sodium-selective and a sustained component. The

XX channels are sensitive to amiloride. The specification describes ASIC3

XX proteins, which are expressed in the sensory neurons but not in the

XX brain. The cation transport channel proteins can be used in methods to

XX identify substances capable of modulating the activity of cation

XX transport channels. The human ASIC3 protein is also an acid sensor,

XX and might play an important role in the detection of lasting pH changes

XX in humans.

SQ Sequence 533 AA;

Query Match

Best Local Similarity 85.8%;

Matches 445; Conservative 49; Mismatches 37; Indels 2; Gaps 2;

Score 2447; DB 21; Length 533;

Pred. No. 5.3e-217;

1 MKPTSGPEEA-RROPDIRFASNCMIGHYFGPSILRGMMAAVLVAVFLVQ 59

1 MKPRSLERQKROASDIRFASCTMIGHYFGPSILRGMMAAVLVAVFLVQ 60

60 VAEVRYEYEFHQTALDERESHRLVPAVTLICNINPLRSRLTPNDLHWGSAALGLDP 119

61 VAEVRYEYEFHQTALDERESHRLVPAVTLICNINPLRSRLTPNDLHWGSAALGLDP 120

120 AEAALALRALGRPARPGPSTFPMALQYARAGSLDMLDCRFRCPCPENVFTT 179

121 AEAALALRALGRPARPGPSTFPMALQYARAGSLDMLDCRYRQPCGPENVFTT 180

180 FTFMGKCYFNAGDAGALLTTRGGMNGDMLDVOOEYLPVWRNDEPFEFGIRV 239

181 FTFMGKCYFNAGDAGALLTTRGGMNGDMLDVOOEYLPVWRNDEPFEFGIRV 240

240 QIHSGEPPILDLGLGVSPGYTFVSCQOQQLSFLPPWGDSSSLNP-NYEPEPSDP 298

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QY 1 MKPTSGPEBA -RRQPSDIREVFASNCMHGLGVFGPGLSLLRGMMAAVLSVATFLYQ 59
DB 1 MKPRSGLEBAQRASDIRVFASCTMGLGHIIFGPGGLTLRGLMATVLLSLAFLYQ 60
QY 60 VAERIRYREFHNOALDERESHRLVFAVYLCNTNPLRSLRTPNDMLMAGSALLGLDP 119
DB 61 VAERIRYREFHNOALDERESHRLVFAVYLCNTNPLRSLRTPNDMLMAGSALLGLDP 120
QY 120 AEHAALYLRALGPPAPPGPMSPPTDMDOLYARAGHSLDDMLDRCRPGCPENFTT 179
DB 121 AEHAALYLRALGPPAPPGPMSPPTDMDOLYARAGHSLDDMLDRCRPGCPENFTT 180
QY 180 FTRMGKCYTFNSGADGAEILLTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPFVEYIRV 239
DB 181 FTRMGKCYTFNSGADGAEILLTTRGCMGNGLEIMLDVQOEYLPVWRDNEETPFVEYIRV 240
QY 240 QIHSGEPPPIIDQLGLGVSPGYQTVSCQOQDLFLPPWGCSSASLNP -NYEPPSPD 298
DB 241 QIHSGDEPPPIIDQLGLGAAPGHQTFVSCQOQDLFLPPWGCNTASLDPDDEPPSPD 300
QY 299 LGSPPSPSPPTTLMGCRACETRIVARCGGRMYMPGDVPCSPQOKKCAHPAIDAI 358
DB 301 LGSPPSPSPPTTLMGCRACETRIVARCGGRMYMPGDVPCSPQOKKCAHPAIDAI 360
QY 359 LRKDSACPNPCASTRYAKELSMVRIPSRAARFLARKLNRESEAYIAENVLALDIFFEAL 418
DB 361 LRKDTVCVPCATRYAKELSMVRIPSRAARFLARKLNRESEAYIAENVLALDIFFEAL 420
QY 419 NYETVEOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDKVGLGYFNNRQHS 478
DB 421 NYEAEVOKKAYEVESELDDIGOMGLFTGASLLTLEILDYCEVFRDKVGLGYFNNRQHS 480
QY 479 ORHSSTNLQEGLSHRTQVPHLSGPRPPCAVTKTSLASHRTCYLVNQL 531
DB 481 ORKSNTLLQEBELNGHRTVPHLSGPRPPCAVTKTSLASHRTCYLVNQL 533

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RESULT 8  
AAM68506  
ID AAM68506 standard; Protein: 512 AA.

AC AAM68506;  
DT 02-FEB-1999 (first entry)

DE Human acid sensing ionic channel MDEC.  
KW Human; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;  
KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;  
KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;  
KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;  
KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;  
KW amyotrophic lateral sclerosis; cerebellar ataxia.

OS Homo sapiens.  
XX  
XX MO9835034-A1.  
XX  
XX PD 13-AUG-1998.  
XX  
XX PE 11-FEB-1998; 98MO-FR00270.  
XX  
XX PR 28-JUL-1997; 97FR-0009587.  
XX  
XX PR 11-FEB-1997; 97FR-0001574.  
XX  
XX PA (CNRS ) CNRS CENT NAT RECH SCT.  
XX  
XX PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M;  
XX Waldmann R, Lingueglia E;  
XX WPI: 1998-447231/38.  
XX DR N-PSDB; AAV60841.  
DR

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XX Protein comprising proton-sensitive neuronal channel - useful for
PT screening for analgesics and for treating neurodegeneration
PS
XX Claim 4: Page 31-33; 64pp; French.
XX
XX This sequence represents the human Acid Sensing Ionic Channel (ASIC)
CC protein MDEC, a member of the neuronal cationic channel family that are
CC sensitive to amiloride and activated by protons. The protein can be
CC used to screen for modulators of these channels, particularly to identify
CC compounds that modulate perception of acidity, as regards nociception
CC (pain) rather than taste. These compounds are used to treat or prevent
CC or some tumours) and as inhibitors of neurodegeneration caused by
CC overexpression of the channels. Antibodies to the protein are used to
CC detect the channels in tissues, and to act therapeutically as channel
CC modulators. The nucleic acid can be used to generate transgenic,
CC particularly knockout, animals for studying ASIC-related disorders,
CC also for gene therapy. The channel protein, or its (ant)agonists, can
CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.
CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
CC sclerosis or cerebellar ataxia.
SQ
Sequence 512 AA:
Query Match 47.9%; Score 1365; DB 19; Length 512;
Best Local Similarity 50.6%; Pred. No. 3,8e-117;
Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;

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122 HAA--FLRALGRPPAPPGPMSPPTDMDOLYARAGHSLDDMLDRCRPGCPENFTT 178  
DB 127 HADPSVLEALRQKANFHYKPK-QFSMLFLRHRYGHDLMKMLCKRGQEGCHQDPTT 185  
QY 179 IFTRMGKCYTFNSGADGAEILLTTRGCMGNGLDIMLDVQOEYLPVWRDNEETPFVEYIR 238  
DB 186 VFTKYGKCYMFNSGEDGKRLTLTVKGTGNGLEIMLDVQOEYLPVWRDNEETPFVEYIR 245  
QY 239 VOIHSQSEPPPIIDQLGLGVSPGYQTVSCQOQDLFLPPWGCSSASLNPYEBSPD 298  
DB 246 VOIHSQSEPPPIIDQLGLGVSPGYQTVSCQOQDLFLPPWGCSSASLNPYEBSPD 298  
QY 299 LGSPPSPSPPTTLMGCRACETRIVARCGGRMYMPGDVPCSPQOKKCAHPAIDAI 358  
DB 299 -----FVYYSIACIIDEETRIYENCNCRWYHMPGDAPFCRPEGNKCAEPALGL 350  
QY 359 LRKDS--CACPNPCASTRYAKELSMVRIPSRAARFLARKLNRESEAYIAENVLALDIFFE 416  
DB 351 AEKDSNYCLCRPCNLTRYNELSMVKIPSTSAVLEKKNFKNSISENIVLIDFIFE 410  
QY 417 ALNVEVOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDKVGLGYFNNRQ 476  
DB 411 ALNVEVOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDKVGLGYFNNRQ 476  
QY 477 HSORHSSTNLQEGLSHRTQVPH 500  
DB 471 DGSIDENVTCTDMPNHSFTISH 494

RESULT 9  
AAM93420  
ID AAM93420 standard; Protein: 512 AA.  
AC AAM93420;  
DT 14-JUN-1999 (first entry)



XX	
DE	Human BNCL protein.
XX	
KW	Human brain sodium channel protein; BNCL; non-voltage dependent;
KW	amloridine sensitive; sodium; lithium; treatment; disease; dysfunction;
KW	central nervous system; psychiatric disease; depression; schizophrenia;
KW	dementia; Alzheimer's Disease; neuronal cell membrane depolarization;
KW	hyperpolarization; autism; dyslexia; seizure; neurotransmitter.
XX	
OS	Homo sapiens.
XX	
PN	US5892018-A.
XX	
PD	06-APR-1999.
XX	
PF	31-MAR-1997; 97US-0828596.
XX	
PR	02-APR-1996; 96US-0072104.
PR	31-MAR-1997; 97US-0828596.
XX	
PA	(PRIC/) PRICE M P.
PA	(WELS/) WELSH M J.
XX	
PI	Price MP, Welsh MJ;
XX	
DR	WPI; 1999-253933/21.
DR	N-PSDB; AAX23167.
XX	
PT	New nucleotide sequence encoding a brain sodium channel protein -
PT	can be used in the development of drugs that modify the activity of
XX	these proteins
PS	Claim 11; Fig 1; 23pp; English.

[illegible]

RESULT 10  
AAV69177  
ID AAV69177 standard; Protein; 512 AA

AC	AAY69177;
XX	
DT	30-MAY-2000 (first entry)

DE A human acid-sensitive cationic channel 2A (hASIC2A).  
XX  
KM Neuronal acid-sensitive cation channel; ASIC; ASIC 2A;  
KM proton-gated cation channel; biphasic desensitisation; amiloride;  
KM cation transport channel; acid sensor; pH detection.

OS	Homo sapiens.			
XX				
XX	WO200008149-A2.			
PN				
XX				
PD	17-FEB-2000.			
XX				
PF	05-AUG-1999;	99WO-1B01445.		
XX				
PR	05-AUG-1998;	98US-0095408.		
XX				
PA	(CNRS ) CNRS CENT NAT RECH SCI			

PI Waldmann R, Bassilana F, Lazdunski M, De Welle JR,  
XX  
DR WPI: 2000-195574/17.  
DR N-PSDB; AA261199.

PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used  
PT to identify substances capable of modulating cation transport channel  
PT activity -  
XX  
PS Disclosure: Page 70-72; 84pp; English.

CC The present sequence represents a human neuronal acid-sensitive cation  
CC channel 2A (ASIC2A) protein. The protein is a proton-gated cation  
CC channel substrate that has biphasic desensitisation kinetics with both  
CC a rapidly inactivating sodium-selective and a sustained component. The  
CC channels are sensitive to amiloride. The specification describes ASIC3  
CC proteins, which are expressed in the sensory neurons but not in the  
CC brain. The cation transport channel proteins can be used in methods to  
CC identify substances capable of modulating the activity of cation  
CC transport channels. The human ASIC3 protein is also an acid sensor,  
CC and might play an important role in the detection of lasting pH changes  
CC in humans.

XX	Acid sensitive ion channel (ASIC) proteins - useful in gene therapy
PT	for treatment of pH mediated pain disorders
PS	Claim 5; Page 43-47; 62pp; English.
XX	This sequence represents an acid sensitive ion channel (ASIC) of the
CC	invention, isolated from rat dorsal root ganglion. Antisense ASIC DNA or
CC	RNA is useful in gene therapy for downregulating expression of ASIC protein,
CC	for pH mediated pain disorders e.g. in Ischaemia. The vectors are useful
CC	for incorporating ASIC DNA or RNA for use in gene therapy. Proton-gated
CC	ion channel agonists and antagonists are identified using cells
CC	transformed with ASIC DNA by allowing interaction between the candidate
CC	substance and ASIC protein in the membrane, and measuring interaction
CC	and/or cell response. Partial agonists and antagonists can be identified
CC	by their ability to block the response of the cell to present in a
CC	solution of a given acid pH or any agonist. The hybridisation probes are
CC	useful for screening libraries for ASIC DNA or RNA.
XX	
Seq	Sequence 513 AA;
Query Match	47.0%; Score 1340; DB 20; Length 513;
Best Local Similarity	49.8%; Pred. No. 7.7e-115;
Matches 256;	Conservative 83; Mismatches 111; Indels 34; Gaps 7;
QY	1 MKPTSGPEARROPSDIKVFVAFNSCMHGLGHVPGSLSLRGMAAAVLVAFTFLYOY 60
DG	1 MEAGSEIDEGDDSPRDLYAFANSCLTGLHAHYVEGGCGPQALMAFAVIALGALCOY 60
QY	61 AERRYRREHFHQALDERESHRLVFRAVYLTCINPLRSKLTPNDLHMAGSALLGDPA 120
DG	61 GDRAAYLYLSYHVTLDEAVATSELVFAVYFNCNNNAVRQLSQLSTYDLYL-APMIGDES 119
QY	121 EHAFLRALGRPPAPGPCFMPSPTEDMALCYRACHSLDDMLDCRFNGOCPGPENFTTIF 180
DG	120 DDPGVPLA---PPGEPAFSGER-FNLIRFYRHSCHRLIEDMLLYSYCGGCPGNFESVF 175
QY	181 TRMGCTYFNSGADGABELITTRKGKMGCLDLMDOOEELPYWRNDETTFEVGIRVO 240
DG	176 TRYRCYTFNSGOGRPRLLTKMKGTGNGLEIMLDIOODETLTPWGETDETSFEAGIKVO 235
QY	241 IHSEEPPIIDOLLAGVSPGYQTFSVSOQQOOLFPLPMGCCSSASLNPNTEPERSDPLG 300
DG	236 IHSDEPFIIDOLFVGAFFGOTFVSCEQRILTYLPSPWGICNAVITMDSP----- 286
QY	301 SPSPSPSPYTLMGCRLACETRIVYARRCGCRMYMPGDVPYCSPOQYKNCAHPAIDAILR 360
DG	287 -----FDYSITACRIDCETRYLVENCNCRMVIMPGDAPCTPEQYKECADPALDFYE 340
QY	361 KDS--CACPNPCASTRAYAKETSWRTISRAARAARLARLKINSLEYIENVALDIFEAL 418
DG	341 KDQEYCCEMPCNLTRIGKELSMWKITSKASAKYLAKFNKSEQYIGNNIIVLDIFFEVL 400
QY	419 NYETVEOKKAYEMSELLDIGOGMGLTGASLTIILEILDYLCIEVFRDKVLGYFWNNQHS 478
DG	401 NYETIQCKAVEINGLIDIGOGMGLTGASIIIVLELFEDYAYEVIKHRLC----RRGKC 456
QY	479 QRHSSTNLDBGLSHRTQVPHLSLGRPPPPC 512
DG	457 QKEAKRSSADKGVA-----ISLDDVKKRHNP 482
RESULT 12	
AAM68507	ID
AAM68507	standard; Protein; 559 AA.
AC	AAW68507;
XX	02-FEB-1999 (first entry)
DT	Rat acid sensing ionic channel 1B.
DE	Rat; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
XW	

KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;  
 KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;  
 KW tumour; cerebral neurodegeneration; pain; taste; inflammation; ischaemia;  
 KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;  
 KW amyotrophic lateral sclerosis; cerebellar ataxia.  
 XX Rattus sp.  
 OS  
 PN MO9835034-A1.  
 XX  
 PD 13-AUG-1998.  
 XX  
 PF 11-FEB-1998; 98WO-FR00270.  
 XX  
 PR 28-JUL-1997; 97FR-0009587.  
 PR 11-FEB-1997; 97FR-0001574.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M;  
 PI Waldmann R, Lingueglia E;  
 DR WPI: 1998-447231/38.  
 DR N-PSDB; AAV60842.  
 XX  
 PT Protein comprising proton-sensitive neuronal channel - useful for  
 PT screening for analgesics and for treating neurodegeneration  
 XX  
 PS Claim 5; Page 34-37; 64pp; French.  
 XX  
 CC This sequence represents the rat Acid Sensing Ionic Channel (ASIC) 1B  
 CC protein, a member of the neuronal cationic channel family that are  
 CC sensitive to amiloride and activated by protons. The protein can be  
 CC used to screen for modulators of these channels, particularly to identify  
 CC compounds that modulate perception of acidity, as regards nociception  
 CC (pain) rather than taste. These compounds are used to treat or prevent  
 CC pain associated with acidity (e.g. in cases of inflammation, ischaemia  
 CC or some tumours) and as inhibitors of neurodegeneration caused by  
 CC overexpression of the channels. Antibodies to the protein are used to  
 CC detect the channels in tissues, and to act therapeutically as channel  
 CC modulators. The nucleic acid can be used to generate transgenic,  
 CC particularly knockout, animals for studying ASIC-related disorders,  
 CC also for gene therapy. The channel protein, or its (ant)agonists, can  
 CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.  
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral  
 CC sclerosis or cerebellar ataxia.  
 CC  
 SQ Sequence 559 AA;  
 Query Match 46.9%; Score 1337; DB 19; Length 559;  
 Best Local Similarity 49.8%; Pred. No. 1.6e-114;  
 Matches 256; Conservative 82; Mismatches 142; Indels 34; Gaps 7;  
 OY 1 MKPTSGPEARARQPSDIRFASNCMHGIGHVFGPGSLRGRGMAAAVAVLSVATFLYGV 60  
 DB 47 MARGSELDEBGDSPRDVLAFAFNSCTFHGASHVFEVGGPPKRALNAVAIVIALGAFLCY 106  
 OY 61 AERYRYREFFHQTALDERESHRLVFPVATLGNINPLRRSRRLTPNDLHWAGSALLGLDPA 120  
 DB 107 GBRVAVYLYSTYPVATLDEVAATELVFAVTCFNTNAVRSLQSLSDYDLVL-APMGLDLS 165  
 OY 121 EHAARLALGRPARPAGFPSPFTFMAQLXARAGSLDMLDCFRQPCGPEPNTTIF 180  
 DB 166 DDPGVPLA---PPGEAFSGEP-FNLHFRYNSCHRLEDMLLYCSYCGGCPGPHNFSYVF 221  
 OY 181 TRMGKCYTFNSGADAEALITTRGGMGNGLDMLDVQCELYPVNRDNEETPFEEVIRVQ 240  
 DB 222 TRYGKCYTFNSGODGRPRKTKMGKGTGNLEIMLDIQODEYILPVNGETDPTSFEGATKQ 281  
 OY 241 IHSQEPPIIDGLGVSPGYOTFVSCQOQSLFPLPPMGDCSSASLNDNPEPSPDLG 300  
 DB 282 IHSODEPPIIDGLGVAVGAFOTFVSCQORLILYLPSPMGTCNAVATYMDSDF----- 332

OY 301 SPSPSPPYTLMGCLACETRYVARKCCRMVYMGDVPVCSPOQYKNCAPDAIDALR 360  
 DB 333 -----FDSYSTACRIDDETRIVENCNCRWVHMGDAPYCTPEYKRCADPAIDFLVE 386  
 OY 361 KDS--CACEPNPCASTRYAKELSMVRIPIPSRAARFLARKINREAVYIAENVLADIFFEAL 418  
 DB 387 KQEVYCVCEMPCNLTRYGKELSMVKIPSKASAKYLAKEFKNSBOYIGENILVYDIFEEVL 446  
 OY 419 NYETVQKKAYEMSELSGIDGOMGLFISASLITLIEILDYLCVPRDQVLYGFYMRKHS 478  
 DB 447 NYETIEQKKAYETAGLIGDGMGLFISASLITVLELFDYAVYEVYIKHRLC---RRGKC 502  
 OY 479 ORHSTNLLQEGLSHRTQVPHLSLGRPPTPC 512  
 DB 503 QKEAKRSSADKGYA-----LSLDVYKRHNPC 528  
 RESULT 13  
 AAY69178  
 ID AAY69178 standard; Protein; 559 AA.  
 XX  
 AC AAY69178;  
 XX  
 DT 30-MAY-2000 (first entry)  
 XX  
 DE A rat acid-sensitive cationic channel 1B (rASIC1B).  
 XX  
 KW Neuronal acid-sensitive cation channel; ASIC; ASIC 1B;  
 KW proton-gated cation channel; biphasic desensitisation; amiloride;  
 KW cation transport channel; acid sensor; pH detection.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200008149-A2.  
 XX  
 PD 17-FEB-2000.  
 XX  
 PF 05-AUG-1999; 99WO-IB01445.  
 XX  
 PR 05-AUG-1998; 98US-0095408.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Waldmann R, Bassilana F, Lazdunski M, De Welle JR;  
 XX  
 DR WPI: 2000-195574/17.  
 DR N-PSDB; AAZ61200.  
 XX  
 PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used  
 PT to identify substances capable of modulating cation transport channel  
 PT activity -  
 PS  
 PS Disclosure: Page 73-76; 84pp; English.  
 XX  
 CC The present sequence represents a rat neuronal acid-sensitive cation  
 CC channel 1B (ASIC1B) protein. The protein is a proton-gated cation  
 CC channel subunit that has biphasic desensitisation kinetics with both  
 CC a rapidly inactivating sodium-selective and a sustained component. The  
 CC channels are sensitive to amiloride. The specification describes ASIC3  
 CC proteins, which are expressed in the sensory neurons but not in the  
 CC brain. The cation transport channel proteins can be used in methods to  
 CC identify substances capable of modulating the activity of cation  
 CC transport channels. The human ASIC3 protein is also an acid sensor,  
 CC and might play an important role in the detection of lasting pH changes  
 CC in humans.  
 CC  
 SQ Sequence 559 AA;  
 Query Match 46.9%; Score 1337; DB 21; Length 559;  
 Best Local Similarity 49.8%; Pred. No. 1.6e-114;  
 Matches 256; Conservative 82; Mismatches 142; Indels 34; Gaps 7;  
 OY 1 MKPTSGPEARARQPSDIRFASNCMHGIGHVFGPGSLRGRGMAAAVAVLSVATFLYGV 60

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[illegible]







**RESULT 2**  
 568434  
 FMRamide-activated sodium channel protein, amiloride-sensitive - brown garden snail  
 C:Species: *Helix aspersa* (brown garden snail)  
 C:Date: 17-Jul-1998 #sequenceRevision 17-Jul-1998 #textChange 24-Sep-1998  
 C:Accession: S68434  
 R:Linguegilla, E.; Champigny, G.; Lazdunski, M.; Bardry, P.  
 Nature 378, 730-733, 1995  
 A:Title: Cloning of the amiloride-sensitive FMRamide peptide-gated sodium channel.  
 A:Reference numbers: S68434; MUID:96107314  
 A:Accession: S68434  
 A:Molecule type: mRNA  
 A:Residues: 1-625 <LINK>  
 A:Cross-references: EMBL:X29113; NID:G1149510; PID:e205469; PID:g1149511  
 C:Keywords: glycoprotein; sodium channel; transmembrane protein  
 F:517-88/Domain: transmembrane #status predicted <TM>  
 F:537-557/Domain: transmembrane #status predicted <TM>  
 F:134,136,303,349,365,372,473/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 419; DB 2; Length 625;  
 Best Local Similarity 22.2%; Pred. No. 1.3e-25;  
 Matches 136; Conservative 99; Mismatches 191; Indels 186; Gaps 20;

Oy	17	IRVFNQNCNMHGLGVNPGPSLSLRGMMAAVYLSVATFLQVAERRYRREFHNOTAL	76
Db	43	IAELGSESNAGLAKIVTSRD-TRKRVIMALLVYLGFTAAATQLSLVLAKYLOFQVELS	101
Oy	77	DERESHRLVFPVATLCINP-----LRR-----SRLPNDLNMGASLGLDPAENHAFPLRA	128
Db	102	EIKDMPQYQPSVSCINLEPISLRTRRMFRNSEQNITWL--RFIOKRFEDQSFMS	159
Oy	139	LGRPPAPGPMSPTF--DMAQLVARAGSLDDMLDCFRGQPCPGPENTTTFT--RMKG	185
Db	160	I-----RAFYENLGQDAKRLSHNLEDMHCRFNRELCHVNSFTFGDGFYFN	207
Oy	186	CYTFSSGADGAEILLTTGGMGNGIDIMLDVQEEYLR-----YMDNDETFEVCIRQI	241
Db	208	CFTFNSG---QRLQMAHATGPNGLSLIFSVKDDPLFGTYGVNFNNILHSHAGVRVYV	263
Oy	242	HSOEPPRIIDGLGVSPQYOTFVSCQOQOLSFLRPPMGDCSSASLN--PNTPEPSPDL	299
Db	264	HAPGMPSPVDHGDIDIPGYSVSSVGLKAILHTRLPYRGNGCTNDMLNIGIKQYK-----	316
Oy	300	GSPSPSPPTTLMGCRACETRYVAKRCGCRMYMPGDV-----	340
Db	317	-----YTFACIQDLQKORLLIQRCGCKSSALP-EVPSYNATFCGVIKMQEINRN	365
Oy	341	-----VCSPOYKNCANPAIDAILKRD-----SCAPNPGCASTR	374
Db	366	HSNEDHNSSEEDRAFIPIPYLACEREOKN-----LNDRIYELSCGCFOPCSETS	416
Oy	375	YAKELSNWRIP-----SRAARFLARKLRSEAYIA-----	405
Db	417	YKSYSLSYMPLEFYQLSAVEREFKQERQAGQNHFMKATVAYEYLEKLANPQKHLARNDSH	476
Oy	406	-----ENVLADIFFEALNTEVEOKKAYEWSSELLGIDGG	440
Db	477	MDDLKSKSYLSSEKEMAKESADLIRQNMRLNITYLEDSLVEYRQLPAYGLADLFADJGG	536
Oy	441	QMGFLIGASLTLTLEIIDYLCEVPKDKVLGFYNNRQ-----HSORHS	482
Db	537	TLGLMGISVLTITHELIELVI-----RLTGLVFNSEKGLPFGPTTVANNNSNNHNSQ-ST	590
Oy	483	STNLLQEGLSGH	494

DB 591 SQHOLYNGYMDH 602

RESULT 3  
S29499  
sodium channel protein alpha chain, epithelial, amiloride-sensitive - rat

C.Species: Rattus norvegicus (Norway rat)  
C.Date: 13-Jan-1995 #sequence,revision 13-Jan-1995 #text\_change 09-Jun-2000  
C.Accession: S29499; S43503; S29715; S41158  
R.Lingueella, E.; Voilley, N.; Waldmann, R.; Lazdunski, M.; Barbry, P.  
PDBS Lett. 318, 95-99, 1993  
A.Title: Expression cloning of an epithelial amiloride-sensitive Na(+) channel. A new  
A.Reference number: S29499; MUID:93170495  
A.Accession: S29499

A.Molecule type: mRNA  
A.Residues: 1-699 <LIN>  
A.Cross-references: EMBL:X70521; NID:9433909; PIDN:CAA49916.1; PID:9433910  
R.Canessa, C.M.  
submitted to the EMBL Data Library, March 1994  
A.Reference number: S43503

A.Accession: S43503  
A.Molecule type: mRNA  
A.Residues: 2-598, 'DV', 601-699 <CAN>  
A.Cross-references: EMBL:X70497; NID:9458845; PIDN:CAA49905.1; PID:9458846  
R.Canessa, C.M.; Horisberger, J.D.; Rossier, B.C.  
Nature 361, 467-470, 1993  
A.Title: Epithelial sodium channel related to proteins involved in neurodegeneration.  
A.Reference number: S29715; MUID:93156815  
A.Accession: S29715

A.Molecule type: mRNA  
A.Residues: 2-194, 'P', 196-230, 'GAA', 234, 'LPAYATIT', 243-598, 'DV', 601-699 <CAN>  
A.Cross-references: EMBL:X70497  
R.Canessa, C.M.; Schild, L.; Buell, G.; Thorens, B.; Gautsch, I.; Horisberger, J.D.;  
Nature 367, 463-467, 1994  
A.Title: Amiloride-sensitive epithelial Na(+) channel is made of three homologous sub  
A.Reference number: S41158; MUID:94150624

A.Contents: annotation  
C.Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I r  
C.Keywords: glycoprotein; sodium channel; transmembrane protein  
F:110-162/Domain: transmembrane #status predicted <TM1>  
F:422-457/Domain: fibronectin type I repeat homology <1FR>  
F:567-613/Domain: transmembrane #status predicted <TM2>  
F:425,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 414.5; DB 2; Length 699;  
Best Local Similarity 22.9%; Pred. No. 3.4e-25;  
Matches 147; Conservative 97; Mismatches 236; Indels 161; Gaps 21;

QY 6 GPE-EARROPD-----IRVPSNCSMHGLHVGPGSLSRGMMAAV 49  
DB 58 GPEPSAPROPTEEEFALIEFHRSYRELFOFCNNNTTIGAIRLCSKHNKTKTFWA--- 114  
QY 50 VLSVATFLYQVAERYRYREF-NHOTALD-FRESHRLVFPVVTLCNINPLRRSR- 102  
DB 115 VLMCTFCGMATWQFALLFEELSYPSVLINLMSDKLVPVAVTCTLNPRYTEKELE 174  
QY 103 -----TPNDLHWAGSALLGLDPAEHAFLRALGRRPAPGPMSPFTDMAOLYARAG 154  
DB 175 ELDRITEQTLFDLYKYNSSTRQAGARRRRSRDLLGAPRPHLQRLRPPTPPYSGRTARSG 234  
QY 155 HS----- 156  
DB 235 SSSVVDNNPQVDRKDWKIGQLCNQNSKDCPYQTYSSGVDAVRWYRHHYINILSR-SDT 294  
QY 157 -----LDMLDCRFRRGQPCGRENFTTLEFRN-GKCYFNSGADAEALLTTGRGMG 207  
DB 295 SPALFEELKGNFTTCRQNPACNOANYSKFNHPYGCITFND-KNNSNLMSSMGVNV 353  
QY 208 NGLDMLDVQOEEELLPVRWDRNEETPFVEGIVQIHSDGEPIIDQLGLGVSPGYQVSC 267  
DB 354 NGLSLTLTFTQENDFIPL-----LSTVYGARVNVHNGDEPRFMDGGGNNLRAPGETSISM 407  
QY 268 QQQQLSFLRPWGDCCSSASLNPNTEPEPSDPLGSPSPSPSPPTLMLGCRCLACETRYIARK 327



```

Db      408  RKREALDLSGMYGDCPT-----ENGSDVPYKNLYPS---KTYGQVCIHSCFQENMTKK 456
OY      328  CGCRRVY--MGDDVPVCSPOQ-----YKNCAHPALDALLRKDSC--ACPNCASRY 375
Db      457  CGCAVIFIPKRGVGEFCYRKQSSMGYCYKLGAFSDSL--GCSKCRKPCPSVINY 512
OY      376  AKELSMVRIPRAAARLARKLRNSEAVIAEN---VLADIFFEALNYETVEOKAYEM 431
Db      513  KLSAGYSRMPVSQSDWTFEEMLSLÖNNYNTINNRKGAVAKLINFEEELMYKTNSESPSYTM 572
OY      432  SELAGDIGGONGLFGAASLTITLETIDYCEV-----PRDYKJGFWMNQHSQR 480
Db      573  VSLSNLGSQMSLWNGSSVLSVEAEALIFDLVLITLMLLRRRSR---YMSFGRGAR 628
OY      481  -----HSTNLDLGBLGSHTQVPHLSLGRPPPPCAVY 515
Db      629  GAREVASTPASSPSRRCPHPTSPR-SLPQGGMTPIALYT 668

```

RESULT 4  
A49585  
Nat channel protein, amiloride-sensitive - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence.revision 16-Feb-1996 #text\_change 09-Jun-2000  
C:Accession: A49585; 151911  
R:Volliay, N.; Linguaglia, E.; Champagny, G.; Mattei, M.G.; Waldmann, R.; Lazdunski, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 247-251, 1994  
A:Title: The lung amiloride-sensitive Nat channel: biophysical properties, pharmacology  
A:Reference number: A49585; MUID:94105144  
A:Accession: A49585  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-669 <RES>  
A:Cross-references: EMBL:X76180; NID:g452649; PIDN:CAAS3773.1; PID:g452650  
R:McDonald, F.J.; Snyder, P.M.; McCray, P.B.  
Am. J. Physiol. 266, L728-L734, 1994  
A:Title: Cloning, expression, and tissue distribution of a human amiloride-sensitive Na  
A:Reference number: 151911; MUID:94295729  
A:Accession: 151911  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-669 <RES>  
A:Cross-references: GB:L29007; NID:g493125; PIDN:AAA21813.1; PID:g493605  
C:Genetics:  
A:Map position: 12p13  
A:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repeat

[illegible]

```

Db      320 SMPG:INNCISLMLRAEQNDIFPL-----LSTVGARVWYHGDEFAFMDDGFFNLRPcy 373
Qy      262 QTFVSCOOOOLSTFPPMDGCSASLNPNEYEPSPD-PLGSPSPSPPTLYLNGCRLAGE 320
Db      374 ETSISMKEETLDRLGVDGDCDK-----NNSDVPEVNLKPS--KITQOVCIHSCF 421
Qy      321 TRYVARKGCRMYWMPGDVPCSPQOYKNCAPALDILRKDS----- 363
Db      422 QESMKEGCAVIFYP-----RQNEYCOY-----RKHSWGVCYKKLVDPSSDH 468
Qy      364 ---CACPNPCASTRYAKELSMVRIPSPBAARFLARLNSEAYIAEN---VLALDIEF 415
Db      469 LGCFTKCRKPCSVNYSYOLASGYSPWPSVTSQEWYFQKLSRQNNYVNNKRNVAKYINFF 528
Qy      416 EALNTEYEQKKAIDMSLLDDIGCGMGLFGASLLTILELIDLYCEV-----F 464
Db      529 KELNCKTSESPPSVYMWVLLTNLSQWMSLWGSVLEVEAMALVPEDLIYIMELMLLRP 588
Qy      465 RDKVLGYWNQNOHOSRHSS---TNLQEGLSHRQOVH---LSLGRPPRPPCAIVTK--- 516
Db      589 RSR---YWSRGGRGGRQOEVAASLTASSPPSH--FCBPMSLSLSQGPASPALTAAPP 642
Qy      517 -----TLASHRTCYL 527
Db      643 AYATLGRPPSPGSGAGASSSTCPL 666

```

RESULT 5  
 T25401  
 hypothetical protein T28B8.5 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T25401  
 R:White, S.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z20029  
 A:Accession: T25401  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-548 <MW>  
 A:Cross-references: EMBL:Z81133; PIDN:CA803443.1; GSPDD:GND0019; CESP:T28B8.5  
 C:Experimental source: clone T28B8  
 C:Genetics:  
 A:Gene: CESP:T28B8.5  
 A:Map position: 1  
 A:Introns: 36/2; 71/3; 105/3; 138/2; 170/3; 196/2; 263/1; 356/1; 383/2; 402/3; 452/3;

	Query Match	14.28;	Score 406;	DB 2;	length 548:	
	Best Local Similarity	23.68;	Pred. No. 1.2e-24;			
	Matches 129;	Conservative 92;	Mismatches 218;	Indels 108;	Gaps 2	
QY	20 FASNCSMHGLGVGPGSLRLRCGMMAAAVVLVAATFLGYOAEVRVRYREHHQTALDER	79				
	:       :       :           :       :					
Db	15 FSCMTSTGVPHI -GMANARMLRAFWLLVVVSIALFTWQFITLITNYLSFSVNTETTLQ	73				
	:       :       :           :       :					
QY	80 ESHRLVPFAVTLCINIPLRRSRLTPNDLHW-----AGSALLGLDPAEHAHA-----	124				
	:       :       :           :       :					
Db	74 FAER-TFFPTVLTCHLNPKKLSETSVDPDMGALIDATNSSSSAQQL-PASLTADHQOQ	131				
	:       :       :           :       :					
QY	125 ---FLRALGRPPAPGEMSPTEFMDAOLYARA-----GHSLDDMLLDICRFR	167				
	:       :       :           :       :					
Db	133 ASKMTLLISDAORAPGTIST--DKSFPEKAKHCXSKLKGLADADIIVSYDDMWVSCSTY	189				
	:       :       :           :       :					
QY	166 GGPCEPENVTTTFE-RMKCYTENSAGNDAGALLTTTGSGMGNGIDLVDVOQEEXYLPIVMR	226				
	:       :       :           :       :					
Db	190 ATCTCITDFENFYNPNSYCNCLQFMF--DG--MYSSSRAGPLLYGLRMWRMDQDTYLP-WT	244				
	:       :       :           :       :					
QY	227 DNEETPFVEGIHVJOHSOEPRIIDQLGLGVSPGYOFVCSOOQQQLSFLPPMGDCSSAS	286				
	:       :       :           :       :					
Db	245 EAS-----GVYIIDHMDELIFPDYGVGYRAPPGTASLGYSVYOTLRSLKPGSCCTTKT	298				
	:       :       :           :       :					
QY	287 --LNDNVPERPSDPLGSFSPSPSPPTLTMCGRCLCETRYVARCKGCGRMVMPGDVPCSP	344				

```

Db 299 KUKTTHY-----TGTYTVEACFRSCMQEKTIASCCG---YYPAYSHASNT 340
Oy 345 QOYKNCAN-----PAIDAILRKDS-----CACPNPCASTRYAKELSVIRPSRA 388
Db 341 TQYVSDNCGVQTLNLNACDNLNSADSTFEDVLTQDCDQPCQPEIDSYGVTVSTAOQMPSPS 400
Oy 389 AARFLARKLN-----RSEA---YIAENVLALDIFEALNVEYBOKKAYEMSELL 435
Db 401 ---YVTECNPGPGSGPMDASGESCLDMYKANTVILEIYERHNFQVLTPESPAYTFVNTI 457
Oy 436 GIGGOMGCFIFASLITILEIDYLCVEVRDKVLYGFMRKQHSQRHSSTNLLQEGIGSHR 495
Db 458 SOVGGOVGQFLGMSIISALE---YVLVLP---LVFEFYCCTKHSRRAEIEOLEMDIKRAK 510
Oy 496 TOVPHLS 502
Db 511 DDYDOVA 517

```

## RESULT 6

```

A54065
sodium transport protein gamma chain - rat
N:Alternate names: sodium channel protein RCNaCH2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jun-2000
C:Accession: A54065; S41160
R:Litueglia, E.; Renard, S.; Waldmann, R.; Volley, N.; Champigny, G.; Plass, H.; Lazdu
J. Biol. Chem. 269, 13736-13739, 1994
A:Title: Different homologous subunits of the amiloride-sensitive Na(+) channel are diff
A:Reference number: A54065; MUID:94245676
A:Accession: A54065
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-650 <LIN>
A:Cross-references: GB:X78034; NID:9495270; PIDN:CA54364.1; PID:9495271
R:Canessa, C.M.; Schild, L.; Buell, G.; Thorens, B.; Gautschi, I.; Horisberger, J.D.; Ro
Nature 367, 463-467, 1994
A:Title: Amiloride-sensitive epithelial Na(+) channel is made of three homologous subun
A:Reference number: S41158; MUID:94150624
A:Accession: S41160
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-52, 'P', 54-572, 'C', 574-650 <CAN>
A:Cross-references: EMBL:X77933; NID:9458849; PIDN:CA54905.1; PID:9458850
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe
F:373-408/Domain: fibronectin type I repeat homology <LFR>

```

```

Query Match 14.0%; Score 398.5; DB 2; Length 650;
Best Local Similarity 23.2%; Pred. No. 6.1e-24;
Matches 154; Conservative 93; Mismatches 233; Indels 183; Gaps 26;

```

```

Oy 3 PTSGGEARROPDSIDRVASNSMGLGHVFGPSLSLRGMAAAYLVSAATFLYQVAE 62
Db 16 PVRGP-QAPPTIKDLNHWCMNTNTHGCRRIYVSRG-RLRRLLIAFTLVAVALIITWQCL 73
Oy 63 RVRYYREFHNOTALDERESH-RLVPAVATLCINPLRHSR---LTPNDLIMAGSALIG 116
Db 74 LV-----FSFYVSISIVKHPOKLDPRAVTICINIPKYKSANSDLLDLDSE-TQALIS 127
Oy 117 LDPAEHAFLRALGRPA-----PPGF---MSPTFD-----MAQL-----Y 150
Db 128 LYGVESRRKRRRAGSMPTLEGTPRPFKFLPLVLFENEKKGARDFTRKRKISKII 187
Oy 146 -----MAQL-----Y 150
Db 188 HKASVNVHVESKLVGFCQNSDTSDCATYTFSSGINAIOEWYKLYHNTIAOYPLEKK 247
Oy 151 ARAGSLDMLDCRFRGQPCGFENFTTIFTRM-GKCYTFNSGADGAEILLTTTRGGMNG 209
Db 248 INMSASABELLYTCFFDGSCDARNFTLPHHMYGNCYTFNN-KENATITLSMKGSEYG 306
Oy 210 LDMLDVQOEEYLPVWRDNETPFEV---GIRVOIHSQEEPIIDOLGLGVSPLYQTFVS 266

```

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Db 307 LOVILYINDEY-----NPFVSSYGAQVYLHOOENEPFIDVGMETIAMSTSIG 357
Oy 267 CQOQOOLFPPMWDCCSASLNPVNEPESDPLSPSPSP---SPPYTLMGRLCETRY 323
Db 358 MLTSEFKLSPEYSOCTED-----GSDVPTNTIYNATISLQICLYSCFQTK 403
Oy 324 VARKGCGRMVY--MPGDVPCSPQOYKN---CAHPAIDAILRKD---SCACPNCASTRY 375
Db 404 IVEKCGCAQYSGPLPRAANYCYQHHPMMYCYQYLOQAFVAREELGCGSVCAQSSPFEM 463
Oy 376 AKELSVIRIPSAARFLA-----RKLNRSEYIAENVLADIFEALNVEY 423
Db 464 TLTTSLAQWPSSEASEKMLNLVLTWDSQOINKKLNKT-----LAKLIFYKLDNRSI 517
Oy 424 EOKKAYEMSELLGIDIGGOMGLFISLITILEIDYLCVEFRDKVLYGF----- 472
Db 518 MESPAHSIEMLSNFGQGLGMLMSSGVVCVETI---EVF---FIDFSIARQMHKA 570
Oy 473 ---WNROHSQRHSSTNLLQEGIGSHR---TQVPHLSIGPR-PPYPPCAVTKTSLASHRT 524
Db 571 KDMWARRQTPPTETPSSRQGDNPALDITDDLPFTFSAMRLPAPAGSVPTPPRYNT 630
Oy 525 CYL 527
Db 631 LRL 633

```

## RESULT 7

```

I51684
epithelial sodium channel, gamma subunit - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jun-2000
C:Accession: I51684
R:Pnuoti, A.; May, A.; Canessa, C.M.; Horisberger, J.
Am. J. Physiol. 269, 188-197, 1995
A:Title: The highly selective, low conductance epithelial sodium channel of Xenopus 1
A:Reference number: I51682
A:Accession: I51684
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-660 <PUD>
A:Cross-references: EMBL:U25342; NID:9886045; PIDN:AAA74972.1; PID:9886046
A:Genetics:
A:Gene: gammaXENac
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I r
F:375-410/Domain: fibronectin type I repeat homology <LFR>

```

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Query Match 13.7%; Score 391.5; DB 2; Length 660;
Best Local Similarity 21.7%; Pred. No. 2.3e-23;
Matches 141; Conservative 105; Mismatches 232; Indels 171; Gaps 23;

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```

Oy 3 PTSGGEARROPDSIDRVASNSMGLGH-VFGPSLSLRGMAAAYLVSAATFLYQVA 61
Db 17 PVTGP-QAPTYELMQWCLNTHGCRRIYVSKG-RLRRWISLTLCAVAAYFWMCA 73
Oy 62 EVRYYREFHNOTALDERESHRLVPAVATLCINPLRHSRL-----TPNDLH 108
Db 74 LLIMSY---YSVASITTYPOKLYPAVATICNLNPIYSISKYKDLALAEKETISQTLKNIY 130
Oy 109 WAGSALL-----GLDPAEHAFLRAL----- 129
Db 131 GFTPELIRSKRDVGVNENSTEDIFLQIDPLRYLESVKSQLVVSDLTKKRTRMSAKVI 190
Oy 130 ---GRPARPGFM-----PSPTFD-----MAQLYAR--- 152
Db 191 HDAESVODPGNMWGFKLCDPRNSSDCITFTSSGVNAIOEWYRLHYNTIAKISMEDKI 250
Oy 153 -AGHSLDMLDCRFRGQPCGFENFTTIFTRM-GKCYTFNSGADGAEILLTTTRGGMNG 210
Db 251 AMGYADELLIYTCFFDGSCDARNFTLPHHPLXGNCYTFNS-AEAGNLLVSMKGAEYGL 309
Oy 211 DIMLDVQOEEYLPVWRDNETPFEV---GIRVOIHSQEEPIIDOLGLGVSPLYQTFVS 270

```

```

Db      310  KVLVIYDEED-----NPIYI$TAAGKILYHODEPFIETLEYETLEFATETISIGMÖLT 363
Qy      271  QLSFLPWPWDCS-----SASLNPIYEEDEPSPDLGSPSPSPPYTLMGCLACETRYVAR 326
Db      364  ESAKISDPYSDCITMDGRVSEYENLYNKK-----YTIQICINSGFQEMVR 408
Qy      327  KCGCRMV--YMPGDVPVCSPOQYN---CAHPAIDAILKRD---SCACNPPACSTRYAKE 378
Db      409  SCGCAHYDQPLPNGAKACNNEEYPSWITCYCFKYKVPQVOCLOCSQSCRESCSEFKMÖTLL 468
Qy      379  LSNVWIPS-----PRAAFELARKINRSEPAVIAEAVULA-IDIFPAPALVEYVEQKRAY 429
Db      469  RSLAKWPSLSEEMWMLRYLSMELGEEKLNKN---LTKMDLNLNITFYÖDLN$RISISSPYT 525
Qy      430  EMSLELGDIGGOMGLFTGASILLITLET-----IDYLCYVRDVKVLGYFMNROHSORH$ST 484
Db      526  NIWTL$NFGQGLMLM$CMSMICVLETTIEVFIDSFWVVL$RQRMWMEKRKNQÖEDPP 585
Qy      485  NILRGELGSH-----RQYVHLSLGRPPRPP 511
Db      586  EIPVPTMIGHDNPLCYVDNPICLGEEDPPTNSALQÖLP$QOSD$SHVPRPP 634

```

```

Db      372 -----| | : : : ||| : ||| | : ::| : |
          -YTEOVCAVRSCHFOAMAVACGGCIAFYFLSPED-QYCDYNKHKSGHCYK 420

Qy      357 AIL-----RKDSC--ACPNCASFTYAKELSWRIPSRAPAAFLARKNRESEAYIAENVLA 410
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      421 LIIEFTSKKLCGFCFKCRPCPLCVSEYOLTAGYSKMPNNVSODWVLHTLSROYNLDRGIA 480

Qy      411 -LDIFFEALNTVEYOKRAYEMSELLDGIGOMGLFGASLITLTLEILDYLCVEYFRDKVL 469
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      481 KNIFFEEELNKTILESEPITMMALLSLIGSOWSLGWSSYLVAWEMLLEVIDFV---II 537

Qy      470 G-----YMNQRHQSRRHSSTNLDEGLSHRTQVPHLSLGRPP-----TPPC 512
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      538 GVMILLHRYYTKKANEGEETTVPTPAPAFADLEQQVPHIDRGDSORQISVVADITPP 597

Qy      513 AVTK-----TLSA-----SHRTCY 526
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      598 AYESLDLRKSVGTLLSRSSSMNSNSTY 624

RESULT 9
151915
```

RESULT 8  
151682  
epithelial sodium channel alpha subunit - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jun-2000  
C:Accession: 151682  
R:Puciti, A.; May, A.; Canessa, C.M.; Horisberger, J.  
Am. J. Physiol. 269, 188-197, 1995  
A:Title: The highly selective, low conductance epithelial sodium channel of *Xenopus laevis*  
A:Reference number: 151682  
A:Accession: 151682  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-632 <PDB>  
C:Cross-references: EMBL:U23535; NID:G968935; PDB:AAA74970.1; PDB:G968936  
C:Genetics:  
A:Gene: alphaENaC  
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repeat  
F:355-390/Domain: fibronectin type I repeat homology <I>

RESULT 9  
 151915  
 epithelial sodium channel beta subunit - human  
 N:Alternate names: sodium channel, nonvoltage-gated 1, beta chain; sodium transport p  
 C:Species: Homo sapiens (man)  
 CjDate: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 17-Nov-2000  
 CjAccession: I51915; I38203; A54986  
 R:McDonald, F.J.; Snyder, P.M.; Price, M.P.; Welsh, M.J.  
 Am. J. Physiol. 268, 1157-1163, 1995  
 A>Title: Cloning and expression of the beta and gamma subunits of the human epithelia  
 A:Reference number: 151915  
 A:Accession: 151915  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-640 <Res>  
 A:Cross-references: GB:L6593; NID:9987622; PIDN:AA75459.1; PID:9987623  
 R:Vollmer, N.; Bassilana, F.; Migon, C.; Merscher, S.; Matzel, M.G.; Carle, G.F.; Laz  
 Genomics 28, 560-565, 1995  
 A>Title: Cloning, chromosomal localization and physical linkage of the beta and gamma  
 A:Reference number: I38203; MUID:96039270  
 A:Accession: I38203  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA

Query Match	13.5%	Score 386;	DB 2;	Length 632;
Best Local Similarity	21.5%	Pred. No. 5.9e-23;		
Matches 135; Conservative	102;	Mismatches 242;	Indels 148;	Gaps 23;

A. Cross-references: EMBL:X87159; NID:gi10042270; PUD:CAA60532.1; PID:gi1004271  
R.Shimkels, R.A.; Warnock, D.G.; Bositis, C.M.; Nelson-Williams, C.; Hansson, J.H.; S

```

0Y 20 FASNC5MGLGHVGPGLSLRRGMOAAAYLVATFLYOVAAERVRVYREFHQTL-D-78
    | | | | | : : : : : | : : : : : | : : : : :
Db 26 FCSNTTHGALRLVCSRRNRKKTFFWLVLYLVYTGMLTWQFG--LIEGQYFSIPVSINL 83
    | | | | | : : : : : | : : : : : | : : : : :
0Y 79 RESHRLVPAVTLNCINIDPLRSRLTPNDLH-----WAGSALLGLDPAEHA 123
    | | | | | : : : : : | : : : : : | : : : : :
Db 84 VNSDKLPAPVATVCLNRYKAI-QNDLQELKEQRTLYELLYKNSTVOGMIINNQR 142
    | | | | | : : : : : | : : : : : | : : : : :
0Y 124 AFLRALGRP-----PAPG-----FMSPT 143
    | | | | | : : : : : | : : : : : | : : : : :
Db 143 VKRDRGLPYLELLELPGESETHRSRSVIEEELQVRRENNIGFKLCNETHGDCFYQYT 202
    | | | | | : : : : : | : : : : : | : : : : :
0Y 144 -----FDMAQLYARA-----GHSDDMLDCCFRRQPCGPEFETITFRM-G-184
    | | | | | : : : : : | : : : : : | : : : : :
Db 203 SGVDAIREMYRFHYINILARPOPAIDBQLENIETPACRFNEESCCKAYNSFHHAIY 262
    | | | | | : : : : : | : : : : : | : : : : :
0Y 185 KCYTFNSG-ABGAELLTTRGCMGNGDIMDYOOEELYLVWMDNETTPREVLSIRQIHS 243
    | | | | | : : : : : | : : : : : | : : : : :
Db 263 NCYTFNOMOSQSNLMWSSMGINGLTLVLRTQHDYIPLSS-----VAAARVLVHG 316
    | | | | | : : : : : | : : : : : | : : : : :
0Y 244 QEEPEIIOOLIGVSPGYQTFVSCQOOOLSLFPMDQC-----SSASINPEPESDPL 299
    | | | | | : : : : : | : : : : : | : : : : :
Db 317 HKEPAFMDNDFNIPGMEJISIGMKKETINRLGKYSIDCSDSDSDVDVKNLFPSE----- 371
    | | | | | : : : : : | : : : : : | : : : : :
0Y 300 GSPSPSPPYTLMGCRILACTETRYVARKCGCRMY----MGDVPVCSPOQYKNCAPHAID 356

```

Cell 79, 407-414, 1994  
A>Title: Liddle's syndrome: heritable human hypertension caused by mutations in the b

A:Reference number: A54986; MUID:95042738  
A:Accession: A54986  
A:Molecule type: DNA  
A:Residues: 515-640 <SH1>  
A:Cross-references: GB:U16023; NID:g563833; PIDN:AAA67036.1; PID:g563833  
A>Note: authors translated the codon GTC for residue 630 as Thr, ATC for residue 631  
C:Genetics:  
A:Gene: beta hENAC; GDB:SCNN1B  
A:Cross-references: GDB:434471; OMIM:600760  
A:Map position: 16p12.2-16p12.1  
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I r

Query Match 13.1%; Score 374.5; DB 2; Length 640;  
Best Local Similarity 22.1%; Pred. No. 5e-22;  
Matches 131; Conservative 93; Mismatches 222; Indels 147; Gaps 22;

OY 20 FASNCSMHGLGHVFGPSGISLRGMAAAVYLVSATFLPYQVAERYRYRFFHQDTALDER 79  
: : | : | : : : | : | : : : :  
Db 29 YCDNTLVTFNHGPKRIICEG--PKKKAMFLLTLLEAFALVCMQGIFIRTYLSWEVSYSLSV- 85  
OY 80 ESHRLVFPAVYLICINPLRSR-----LTPDDLH-----W 109  
: : |||||:| : : | : : | : | : | :  
Db 86 GKRTDPFTVYCNA SPKRYSKIKHLKDLDLMFAVLERILAPELSHANNATRNLFNSIW 145

```

Oy 110 AGSALLGLDP-----AEHAFLRALGRPPAP 136
Db 146 NHTPLVLIDERNPHVPLVDFGDHNGNLSSASEKIONAMGCKMAMRLSLNRQCF 205
Oy 137 GFMSPRTDMDQLYARAGHSL-----DMLDCRRGQPCPEPNTTIF 180
Db 206 RNFATATALTEWYIILQATNIFAQVPOOELVEMSYPGEOMLIACLFGEAPCNYRNFTSTIF 265
Oy 181 -TRMCKCTFNSGADGACELLTTTRGGMNGLDIMLDVOOEYLPLWRDRELPFEVGTIV 239
Db 266 YPHYNCITFIEMNGMT-EKALPSPANGTEFGLKLLIDIGQEDVPLAST-----AGVNL 318
Oy 240 QIHSGEPPRIIDQLGVSPGYQTVSCQOQQLSFLPPWGDSSASLNPYEPEPSDPL 299
Db 319 MLHEGRSVPTFIDEQIYPMSCFETSIGVLVDKLRMNGEYSYC-----TYN----- 364
Oy 300 GSPSP-----SPSPPTLMGCRCLACETRYVARKCCG-RMYV-MPGDVPVCSPOQKNC 351
Db 365 GSEVFNQNFSDYNTYTSIOACLRSQFODHMRNCNCGHYLPPLRGEKCYNNRDPDMA 424
Oy 352 HPAID---ALLRKDSC--ACPNPCASTRYAKELSMVRIPSRRAARFLARKLNSE----- 401
Db 425 HCYSLQMSVMORETICMGKESCNDTQKMTISMADMPSEASEDMIFRHVLSQERDQSTN 484
Oy 402 -AYIAENVLALDIFFEALNRYETVEOKKAYEMSELGIDIGOMGLFISGLTILEILDYL 460
Db 485 ILSRKGIYKLNIFFOEQRNRYIEESANNIYMLSLNGQGFPMGGSVLCLE----- 539
Oy 461 CEVFDKVLGTFWNRHOSHSTNL-----IQEGLSHRTQVPHLSLGRPPT 509
Db 540 ---FGEIITDFW-----ITIKLVALKSLRRRAQASY--AGP-PPT 577

```

## RESULT 10

Sodium transport protein beta chain - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jun-2000  
 C/Accession: S41159  
 R:Caenessa, C.M.; Schild, L.; Buell, G.; Thorens, B.; Gautschi, I.; Holsberger, J.D.; RC  
 Nature 367, 463-467, 1994  
 A:Title: Amiloride-sensitive epithelial Na(+) channel is made of three homologous subun  
 A:Reference number: S41158; MUID:94150624  
 A:Accession: S41159  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <CAN>  
 A:Cross-references: EMBL:X77932  
 C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe

Query Match 13.1%; Score 373; DB 2; Length 638;  
 Best Local Similarity 21.4%; Pred. No. 6.6e-22;  
 Matches 129; Conservative 100; Mismatches 23; Indels 140; Gaps 23;

```

Oy 20 FASCSMHGLGHVPGSLSLRGMAAAVLSVATFLYQVAERYRYREEHHQTALDER 79
Db 29 YCNNTNTGPRRIICEG--PKKAMMFLTLTFLACLVCMQGVETIOTLSWEVSLSM 85
Oy 80 ESHRLVPAVTLNINPLRSR-----LTPDLH-----W 109
Db 86 GFKTNFPAVTVCSNPPQYSKVKHLKDLKYLMEAVLDKLLAKSSHTNTSTLNFTIY 145
Oy 110 AGSALLGLDP---AEHAFLRALG---RPPAPGF----- 138
Db 146 NHTPLVLIDERNPHVPLVDFGDHNSNSNPASTCNAOGCKVAMRLCSANGVCTFRN 205
Oy 139 MPSPEFDMAQLY-----ARAGSLDMLLDCRRGQPCPEPNTTIF-T 181
Db 206 FTSATQATTEWYIILQATNIFAQVPODLYVGMYADRIITLACLETGECSSHRNFTPIYP 265
Oy 182 RMGICYNPSGADGACELLTTTRGGMNGLDIMLDVOOEYLPLWRDRELPFEVGTIV 241
Db 266 DYGCYIFNMGT-EKALPSPANGTEFGLKLLIDIGQEDVPLAST-----AGARLML 318

```

```

Oy 242 HSQEEPPRIIDQLGVSPGYQTVSCQOQQLSFLPPWGDSSASLNPYEPEPSDPLGS 301
Db 319 HQERTYPTFIEGITYAMAGTETISIGVLDKLOGKEPTSPCTMNSDVALQVLYSD----- 374
Oy 302 PSPSPSPPTLMGCRCLACETRYVARKCCG-RMYV-MPGDVPVCSPOQKNCAPDAID--- 356
Db 375 ---YNTYTSIQACLSHSCFODHMRNCNCGHYLPPLRGEKCYNNRDPDMAVLYSLQ 430
Oy 357 ALLRKDSC--ACPNPCASTRYAKELSMVRIPSRRAARFLARKLNSE-----ATIAENV 408
Db 431 SVVORETCLSMKESCNDTQYKMTISMADWPSEASEDMILHVLQERDQSSNITLSRGI 490
Oy 409 LALDIFFEALNRYETVEOKKAYEMSELGIDIGOMGLFISGLTILEILDYLCEVFRQV 468
Db 491 VLNITYFOEFNRYRTIEESANNIYMLSLNGQGFPMGGSVLCLE-----FGEIT 542
Oy 469 LGYFNWRHOSHSTNLQ-----EGLSHRTQVPHLSLGRPPTPCAVTKTLSASHR 523
Db 543 IDFIW-----ITYIKLVASCKGLRRRRQRPY--TGP-PPT-----VAELVEAHT 584
Oy 524 TC 525
Db 585 NC 586

```

## RESULT 11

Protein T28F2.7 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C/Accession: D87739  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
 A:Accession: D87739  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-630 <STO>  
 A:Cross-references: GB:chr\_I; PID:AB53057.1; PID:g2047351; GSPDB:GN00019; CESP:T28F  
 A:Gene: T28F2.7  
 A:Map position: 1

Query Match 13.0%; Score 372; DB 2; Length 630;  
 Best Local Similarity 25.1%; Pred. No. 7.8e-22;  
 Matches 145; Conservative 92; Mismatches 23; Indels 108; Gaps 26;

```

Oy 1 MKPTGPREARROPDIRVPASNCMHGLGHVPGSLSLRGMAAAVLSVATFLYQV 60
Db 12 LKPS-----KRSQILVDPVAHLRIKITEGVSTTRSEHFSSVWFSPESLYNA 65
Oy 61 AERYVYREFHQTALDERSH-----RLVPAVTLNINPLRSRLRP-NDLHWAG 111
Db 66 TQ-QHYVVLNGYTVV--KDGHSFLLSEGGMOFPRVTVCSFNPIKRTVEALNSTKOLS 121
Oy 112 SALLGLDPAEHAFLRALGRPPAP-----PEFMS-PTFMDAQLYARAGHSLDML 161
Db 122 DDLIDYLMFNSSDAMTLTGRDAASLSHSGDNVFKIYVSSHNFATDNFMDAGFSCGMF 181
Oy 162 LDCRPGOP---CGPENTTIFTRGKCTYFN-SGADAELLTTTRGGMNGLDIMLDVQ 217
Db 182 KMSFGGRFPDCC--KYATPIFSDLGKCFITLNGQSDKSMKMKOTEPDIAAGLQIILDSH 239
Oy 218 QEEYLPVWRDNEE--TP-----FEVGIRVOHSQEEPPRIIDQLGVSPGYQTVSCQ 269
Db 240 LEEGF---DSETDGVTVFSSAFENGFRFYTHSEELPFLASGIAVSPSVYVALSS 295
Oy 270 QQLSFLPP-PWGDCSSASLNPYEPEPSDPLGSPSPSPPTTLMGCLACETRYVARKC 328

```

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Db 296 SKYILLSSNANGCSD-----SWPRGY---DYSEPTYSAMCTSMCKAQYFQNL 341
Qy 329 GCR-MY-----MPGDVPVCSPOQYKNCANPAIDALIRKDS-CAPNPGASTRYAK 377
Db 342 GCSPTSYNHLNRNDCTPEYFCMDTKMKKYVNSFN--IEMPTCECKVECKSOYHS 399
Qy 378 ELSMVAIPRAAARFLARKLNSEA---YIAENVLALDIFFEALNYEVEOKKAEEMSE 433
Db 400 FNSYGGKLSRGALMLWT-KQKQETWTIPMKLNPOVAVVFPDMSTYETICKRGSLTE 458
Qy 434 LSGDIGGKGLFTGASLTITLITLIDYCEV---FROKVLGYFWNRQHSQ----- 479
Db 459 LLSDIGNGMGFMGMSVFTIIEFLFLSKIGWIGFSRKRDRDYWSKKKNEMEKELEDY 518
Qy 480 -----RHSST---NLQOE---GLGSHRTQVPHSL 503
Db 519 VTGFKLFRHRKSGKDMSHREKIKGLSMHRVYSEQLNV 556

```

## RESULT 12

T15144

hypothetical protein T28F2.7 - Caenorhabditis elegans (fragment)

C.Species: Caenorhabditis elegans

C.Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C.Accession: T15144

R.Madsen, C.; Fronick, B.

submitted to the EMBL Data Library, April 1997

A.Description: The sequence of C. elegans cosmid T28F2.

A.Reference number: Z18300

A.Accession: T15144

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-630 &lt;MAD&gt;

A.Cross-references: EMBL:AF00198; NID:g2047345; PID:g2047351; PIDN:AA05057.1; GSPDB:GN

A.Experimental source: strain Bristol N2; clone T28F2

C.Genetics:

A:Gene: CESP:T28F2.7

A:Map position: 1

A:introns: 65/3; 83/3; 113/1; 174/2; 353/1; 430/2; 538/2

Query Match 13.0%; Score 372; DB 2; Length 630;

Best Local Similarity 25.1%; Pred. No. 7.8e-22;

Matches 145; Conservative 92; Mismatches 233; Indels 108; Gaps 26;

```

Qy 1 MKPTSPPEARARQPSDIRFASNCMHGHNVPGLSLIRKMAAAVVLVATFLYQY 60
Db 12 LKRF-----KRSQILYDVPYAHLRKIKNTGVSITRESEHFSKWFSEESLYNA 65
Qy 61 AERVRYREPHHOTALDERESH-----RLVEPAVTLTCLNINPLRSRLTP-NDLHMAG 111
Db 66 TQ-QHYWNLNGTYW--KDGHYSLFSLSEGGMQFPVYVCSFNPDKRTTYEALNSTKDS 121
Qy 112 SALLGIDPAEHAFLRALGRPPAP-----PGFMPS-PTPDMQLYARAGSLDDML 161
Db 122 DDLDDYLVAMFNSDPAWTLGYGADAASLHSGDNVFKHYVSSHPNTAANFMDAFCSDGMF 181
Qy 162 LDCRFGRQ---CGPENFTTITRMKCYTFN-SGADGAEELLTTTRGKMGNGLDIMLDYQ 217
Db 182 KMSFSGRREDDC--KYAATPFIIDLCFTLNLQSGDKSMKMQTPEGIAGAIQIILDSH 239
Qy 218 QEYELVWMDNEE--TP-----FEVGIROIHSEEPPIIDQIGVSPGYQTFVSCQ 269
Db 240 LEEQF-----DSETGVTPVFSFAFENGFRFYIHSSEIIPFLASGIAVSDSVVYSLS 295
Qy 270 QQLSFLPP-PWGDSSASLNPNYEPSPDLGSPSPSPPTLMCRLACETRYVYARK 328
Db 296 SKYILLSSNANGCSD-----SWPRGY---DYSEPTYSAMCTSMCKAQYFQNL 341
Qy 329 GCR-MY-----MPGDVPVCSPOQYKNCANPAIDALIRKDS-CAPNPGASTRYAK 377
Db 342 GCSPTSYNHLNRNDCTPEYFCMDTKMKKYVNSFN--IEMPTCECKVECKSOYHS 399
Qy 378 ELSMVAIPRAAARFLARKLNSEA---YIAENVLALDIFFEALNYEVEOKKAEEMSE 433

```

```

Db 400 FNSYGGKLSRGALMLWT-KQKQETWTIPMKLNPOVAVVFPDMSTYETICKRGSLTE 458
Qy 434 LSGDIGGKGLFTGASLTITLITLIDYCEV---FROKVLGYFWNRQHSQ----- 479
Db 459 LLSDIGNGMGFMGMSVFTIIEFLFLSKIGWIGFSRKRDRDYWSKKKNEMEKELEDY 518
Qy 480 -----RHSST---NLQOE---GLGSHRTQVPHSL 503
Db 519 VTGFKLFRHRKSGKDMSHREKIKGLSMHRVYSEQLNV 556

```

## RESULT 13

T25700

mechanosensory protein 10 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000

C.Accession: T25700; S42224

R.Fulton, B.

submitted to the EMBL Data Library, August 1996

A.Description: The sequence of C. elegans cosmid F16F9.

A.Reference number: Z20071

A.Accession: T25700

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-724 &lt;FNU&gt;

A.Cross-references: EMBL:U67956; PIDN:AA07694.1; GSPDB:GN00028; CESP:mec-10

A.Experimental source: strain Bristol N2; clone F16F9

R.Huang, M.; Chalfie, M.

Nature 367, 467-470, 1994

A.Title: Gene interactions affecting mechanosensory transduction in Caenorhabditis el

A.Reference number: S42224; MUID:94150625

A.Accession: S42224

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-724 &lt;HUA&gt;

A.Cross-references: EMBL:L25312; NID:g414798; PIDN:AA017404.1; PID:g414799

C.Genetics:

A:Gene: mec-10

A:Map position: X

A:introns: 90/2; 121/2; 162/1; 189/3; 288/3; 312/1; 337/3; 368/3; 396/2; 421/2; 455/1

Query Match 12.5%; Score 356; DB 2; Length 724;

Best Local Similarity 20.8%; Pred. No. 1.8e-20;

Matches 138; Conservative 82; Mismatches 205; Indels 240; Gaps 22;

```

Qy 17 IRVFASNCMHGHNVPGLSLIRKMAAAVVLVATFLYQYARVRYREPHHOTAL 76
Db 97 LQOFCKYKTSHG-I-PMLGQAPNSLYRAAWFLLLCALQFINQAVAVIQYQKMDKITDI 155
Qy 77 DERESHRLVPAVTLTCLNINPLRSRLTPNDLHMAGSALLGL----- 117
Db 156 -QLKFTAPPAITLCLNLNPKYKDSVIRSHD---SISKILGVFYSVMKKAQSSSEALEEB 211
Qy 118 -----DPA----- 120
Db 212 ETEYVMNGITTOAKRRKRGAGEKGTPEPANSACEDEEDGSECEBERSTKEPSGNDMC 271
Qy 121 ----- 120
Db 272 ICAFDQOTNDAMPCHRRKEQWNTTTCQDDEHLYCSKAKKGTFRSELKKEPCICESKGLF 331
Qy 121 -----EHAFL-----RALGRPPAPPGF----- 138
Db 332 CIKHEHAAMVNLMEYFGSEDESEISTEBEREA-----GFGNMTDEVAIVTKAKENI 384
Qy 139 ---MSPTEPMAQLYARAGSLDDMLDCFRGQPCG-PENFTTIP-TRMGKCYTFNSGA 193
Db 385 IFMMSALSEQRLMSQAKHNL---IHKCSFNKPCDDIDQDEFILVADPTFGKCFVNH-- 439
Qy 194 DGAELLTTTRGKMGNGLDIMLDYQOEYLPVWMDNEETPEVGIROIHSEEPPIIDOL 253
Db 440 DREIFKSSVARGQYGLRVMLFVNASDYLP-----TSAVGIRLTIHDKDFPPDF 492

```

Oy	254	GLGVSPGQTFVSCOOOOLFLRPPMGDCSSALNNYEEBPDJLGSFSPSPRPPTLM	313
Dd	493	GYSAPGTGISFCGRMKRMKMSLRHPYDCCDECATSYIYK-----GYATSE	540
Oy	314	GCRLACETRYVARKCCKGRMYMP--GDVPYCS--POOLKNCAHP--AIDAILRKDSCAC	366
Dd	541	GCYRTCFQELIIDRCGSDPRFPISIGVGPCQYFNKNHRECEKHHTQGEIHGSPKRC	600
Oy	367	PNPGASTRYAKELSMVAIPBSRAARPL-----ARKLNSEAIAENVLAIDIFPEALNY	420
Dd	601	QOPCNOTTYTTSYSAAIWPSQALNISLGOCERKAEBECN--EEV-KENAMLEVFYEALNF	657
Oy	421	ETVEOKRAYEMSELLDGIGSGMGLFTIASLLITLEILDYLCIEVFR--DKVLGFYNRRQHS	478
Dd	658	EVLSESEAYGIYKMMAFDGGHLIGMSVSVMTCCE--FVCLAFELITYAIIAHHTNQORI	714
Oy	479	QRHSS 483	
Dd	715	RRREN 719	

RESULT 14  
 T20420  
 hypothetical protein E02H4.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000  
 C:Accession: T20420  
 R:Barlow, K.  
 submitted to the EMBL Data Library, November 1995  
 A:Accession: T20420  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-664 <M11>  
 A:Cross-references: EMBL:Z68003; P1DN:CAA91975.1; GSPDB:GN00028; CESP:E02H4.1  
 A:Experimental source: clone E02H4  
 C:Genetics:  
 A:Gene: CESP:E02H4.1  
 A:Map position: X  
 A:Introns: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5  
 C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repeat

Query Match	12.48;	Score 353;	DB 2;	Length 664;
Best Local Similarity	25.78;	Pred. No. 2.8e-20;		
Matches 98;	Conservative 61;	Mismatches 145;	Indels 77;	Gaps 13;

```

0Y 148 QLVARAGISLDDMLDRFRGPOCGPENFTTF-----TMGKCYFNSACDAELTTT 202
Db 325 QRRALGYSKELLKMSFNGOC---NIDTERKLHDSFGMCYTFN-ANERKLASS 379
0Y 203 RGGNGSLDIDLMDQOEELPWHRDNEETPEFVGIRVOJHJOEPTLIDLGIVSPGYO 262
Db 380 RAGPSYGLRMLMFVNSDYLP-----TEATGVRIAHGKECEPDPDFGSAPTYI 432
0Y 263 TFVSCQOQOQLFLRPPMGDC-----SSALNTNYPEEPDPLGSPSPSPPTLMGCR 316
Db 433 SSFGISLNLNIRLPOPGNCLQKDNPOSRIYGYKYEPE-----GCF 475
0Y 317 LACETRYVARKCGRCMYMPEGDVPCVCSPOOY-----NCAPHALDILRKSS 363
Db 476 RSCYQYRIAKGCG-----ADPRPKRMKNSAMCDSNTTTLNCLTTEGAKKLTKEN 527
0Y 364 ---CACRPPCASYRAKELSWRIPSAARFLARKLNSEAYIAENVALDIEFALNY 420
Db 528 OKHKCJLOPCOODYTTTYSNAKKPSSIOSCDNHSKDCNSLREHAMIEIYYEOMSY 587
0Y 421 ETEOKKAYEMSELLDPIGGOMGFICASLTLTIELIDYCEVFRKXVGYF-----NWR 475
Db 588 EILWSESYSHFNLMADMGOGAGLFLGASIMSYIEFL-----FFAVRTGLACKPPRR-R 641
0Y 476 QHSO--RHSSTNLQEGLSGH 494
::: :::::

```

Db 642 QKTELLRAEELNDAEKGVSTN 662

## RESULT 15

hypothetical protein R13A1.4 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T16737

submitted to the EMBL Data Library, November 1995.  
 A:Description: The sequence of C. elegans cosmid R13A1.  
 A:Reference number: 218569  
 A:Accession: T16737  
 A:Status: preliminary: translated from GR/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-37 <DUZ>  
 A:Cross-references: EMBL:U40798; NID:g1065928; PID:g1065929; PIDN:AAA81473.1; CESP:R13A1.4  
 C:Genetics:  
 A:Gene: CESP:R13A1.4  
 A:Introns: 30/3; 80/2; 128/1; 155/3; 186/2; 232/3; 261/3; 307/3; 341/3; 394/2; 428/1;

Query Match	12.3%	Score 351;	DB 2;	Length 737;
Best Local Similarity	10.7%	Pred. No. 4.6e 20;		
Matches 144;	Conservative 89;	Mismatches 222;	Indels 276;	Gaps 26

```

42 TTSRSLSSQIDHHTTTTISLAFDPCARTSSHOIPVATSSFFG-----RYMAALF 94
50 VLSVATPELYQAEBVRYYREFNHOTAD-ERESHRLVEFPAVTLNINPLRSRLT----- 1033
95 MCMIAFLLOQYWMSELYQ-RTIEMQLOFAAAMPATATONLNAFYSELQYEEI 152
104 ----- 103
153 KEGFDEWERYINARMSDSMKPGGDILEAISVRKKRSKDOLLFPIDEDLEGAYOPV 212
104 -----PN-----DLHW-----AGALLGD 118
213 FVRCTCMNEOCVNRNRPLEVNASICACFEDYTRGLIWPCTPIPSVWTVKKSCCSISNTC 272
119 P-----AEHAALRAL-----GRPPAPGF 138
273 PDPGPNAKQIAHNHSPRLPCLQGISHCVMHPRKDEIRMMNPNNTYVSVEPPTTEIT 332
139 MPSPFDMAOL-----YARGHSLDMLDCRRRGORCPG 173
333 ETBEAFGLSDLKADGATTTOTKENLIFVALAPRETRRNLSYTLNLEFVLSCFENSKDCSM 392
174 ENFTTFI-FMGKCYTFENSGADGAEILTTTTCGCMGDLIMLDVYOEEELPVMWNEET 231
393 ERDKLIHVDPEYGCYTFENR-DSVE-LKSRAGPMGLKILLNLVHOSDTMP-----T 443
232 PFEVGIRVOIHSQEPRLIDQLGLGVSXGYQTFVSCOOQOLSLFPRMGDCSSA----- 285
444 TEAGGVRLVHEQOQEPDPPTFGVSADPTGFISSHGLKTELHRLSAPMGCSDTFRPVRY 503
286 SLNRYNEPEPSDPLGSSPSPTTYTLMGCRCLACETYYVARKCGCRANVYMPGDVPCSP- 344
504 IYNHYSPE-----GCHRNCFOLKLEIIGC-----GDRPRLPS 538
345 QOYKNC-AHPAID-----AILRKDS-----CACPNPCASTRYAKELSMVPIPSR----- 387
539 EEHHCNKKSXTIDQCSLNTSDSGYHNHLHBOCECQOPHEVEVFETANASAMPSONK 598
388 -AAARFLAKLNKSEA-----YIAENYALDIFFEALYETVEBOKAYEMSELLGDIGOM 442
599 IGTGCPAVSDIENFTACTEYIRNFTXIIIEYBQALNFESLKTACTAGTLYVNLFSDBGNI 658
443 GLFTGASLLTLELDYLCVFR-----DKVLGYFMNRHOSHSSTYNLLOBGJSHRTQVP 499
659 GLMTGFSVITFAEAEALFECECKLMYERKGYIYVOKKMGKEYYSISM-----HID 709

```

OY 500 HUSIGRPPTP 510  
| | : |  
Db 710 FLQRSPKXSP 720

Search completed: October 11, 2002, 07:27:27  
Job time : 56 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 11, 2002, 04:20:18 ; Search time 35 Seconds

(without alignments)  
587.431 Million cell updates/sec

Title: US-09-530-233-2  
Sequence: 1 MKPTSGPEEARQPSDINVF.....CAVKTLSASHRTCTVLTQL 531

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: **SwissProt 40**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1369	40.0	512	1	BNA1_RAT
2	1365	47.9	512	1	Q16515 homo sapien
3	1329	46.6	526	1	BNA2_RAT
4	1298	45.5	574	1	BNA2_HUMAN
5	420.5	14.7	699	1	SCAA_MOUSE
6	419	14.7	625	1	PANA_HELAS
7	417	14.6	646	1	SCB2_XENLA
8	415.5	14.6	647	1	SCAB_XENLA
9	414.5	14.5	698	1	SCAA_RAT
10	407.5	14.3	669	1	SCAA_HUMAN
11	400	14.0	650	1	SCAA_BOVIN
12	398.5	14.0	650	1	SCAG_RAT
13	392	13.7	640	1	SCAA_RABIT
14	391.5	13.7	660	1	SCAG_XENLA
15	391	13.7	655	1	SCAG_MOUSE
16	386	13.5	632	1	SCAA_XENLA
17	384	13.5	653	1	SCAG_RABIT
18	383	13.4	637	1	SCAA_CHICK
19	381	13.4	663	1	SCG2_XENLA
20	379	13.3	641	1	SCAB_RABIT
21	375	13.2	638	1	SCAB_MOUSE
22	373.5	13.1	640	1	SCAB_HUMAN
23	372	13.0	638	1	SCAB_RAT
24	356	12.5	724	1	ME10_CAEEL
25	353	12.4	664	1	DELL_CAEEL
26	351	12.3	777	1	UNC8_CAEEL
27	346	12.1	649	1	SCAG_HUMAN
28	342.5	12.0	768	1	MEC4_CAEEL
29	337.5	11.8	545	1	DEGM_CAEEL
30	336	11.8	795	1	DEGM_CAEEL
31	335.5	11.8	769	1	MEC4_CAEEL
32	326.5	11.5	849	1	DEGM_CAEEL
33	320.5	11.2	638	1	SCAD_PANTR

34	315.5	11.1	638	1	SCAD_HUMAN	P51172 homo sapien
35	310.5	10.9	273	1	SCAB_RANCA	O9w754 rana catesb
36	309	10.8	778	1	DEG1_CAEEL	P24585 caenorhabdi
37	246	8.6	978	1	YSX7_CAEEL	Q10025 caenorhabdi
38	107	3.8	699	1	ATFB_MOUSE	O35451 mus musculu
39	105	3.7	2459	1	MAPB_RAT	P15205 rattus norv
40	104.5	3.7	433	1	ENO4_ANAPL	P19140 anas platyr
41	103	3.6	1739	1	CHD2_HUMAN	O14647 homo sapien
42	102.5	3.6	433	1	ENO4_CHICK	P51813 gallus gall
43	100.5	3.5	2476	1	ZAN_PIG	Q28983 sus scrofa
44	100	3.5	1403	1	CIC_DROME	O9u10 drosophila
45	98.5	3.5	433	1	ENO4_TRASC	O9w711 tracheys s

## ALIGNMENTS

RESULT 1	ID	BNAL_RAT	STANDARD:	PRT:	512 AA.
AC	BNAL_RAT	Q62962;			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Amiloride-sensitive brain sodium channel BNCL1 (Amiloride-sensitive cation channel neuronal 1) (BNCL1) (Degenerin channel MDEG).				
DE	cation channel neuronal 1) (BNCL1) (Degenerin channel MDEG).				
GN	ACCN1 OR BNAC1 OR MDEG.				
OS	Rattus norvegicus (Rat).				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=96209957; PubMed=8631835;				
RA	Waldmann R., Champigny G., Voilley N., Lazdunski M.;				
RT	The mammalian degenerin MDEG, an amiloride-sensitive cation channel activated by mutations causing neurodegeneration in Caenorhabditis elegans. Biol. Chem. 271:10433-10436(1996).				
RT	FUNCTION: NON-VOLTAGE-GATED AMILORIDE-SENSITIVE CATION CHANNEL PERMEABLE FOR SODIUM, POTASSIUM AND LITHIUM.				
CC	SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: BRAIN AND NEURONS.				
CC	- DEVELOPMENTAL STAGE: APPEARS JUST BEFORE BIRTH, REACHES MAXIMUM LEVELS AFTER BIRTH, THEN DECLINES SLIGHTLY UNTIL ADULTHOOD.				
CC	- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS FAMILY.				
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DR	EMBL: U53211; AAC52588.1; -				
DR	InterPro: IPR001873; ASC.				
DR	Pfam: PF00858; ASC; 1.				
DR	PROSITE: PS01206; ASC; 1.				
KW	Ionic channel; Transmembrane; Ion transport; Glycoprotein.				
FT	DOMAIN	1	37		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	38	58		POTENTIAL.
FT	DOMAIN	59	427		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	428	448		POTENTIAL.
FT	DOMAIN	449	512		CYTOPLASMIC (POTENTIAL).
FT	POLY-GLU	469	472		POLY-GLU.
FT	CARBOHYD	365	365		N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD	392	392		G-SS: NO CONSTRUCTIVE ACTIVATION.
FT	MUTAGEN	430	430		G->C: PARTIAL ACTIVATION.
FT	MUTAGEN	430	430		G->F,K,T,V: CONSTITUTIVE ACTIVATION
FT	MUTAGEN	430	430		

FT	MUTAGEN	443	443	48.0%	Score 1369; DB 1; Length 512;
FT	SEQUENCE	512 AA:	57739 MM:	3800A077C3C430B03 CRC64;	S->F: INACTIVATION OF BNAC1 G(430)F.
SQL	SEQUENCE	512 AA:	57739 MM:	3800A077C3C430B03 CRC64;	
Query Match	Best Local Similarity	50.8%			
Matches	256; Conservative	82;	Mismatches 140;	Indels 26;	Gaps 5
QY	7	PEPARQPSDRIYFVNSCMHGLGHVFGGSLSRGMAAAVVLVSATFLYQVAERVK	66		
DB	7	PEEGSLQPSISIOIFANTSTLHGIRHIFVYGPPLIRRVLAVAFVSGILGLLVESSEYRSV	66		
QY	67	YREFHQOTLDRSHRLVFPVATTCNINPLRRSRTLPMDLHWAGSALLGLD----	121		
DB	67	YRSYQHTKVDENVVQSLVFPVATTCNINLGNFRSRLTTMDLTHAGELLALLVNIQIDPP	126		
QY	122	HAA--FLRALGRPAAPGFMPSPTFDMAQLYARAGHSIDMLDLCRFGRQCPGPEFTT	178		
DB	127	HLADPTLVLEALNQKANKFKIKRK-QESMLEFLHRVGHDLKDMMLVKCFKQEGCHQDFTT	185		
QY	179	ITTRMGKCYTFENSGADGAELTTTRGKGNGLDIMLDVQOEYLVPWRDNEETPREVGIR	238		
DB	186	VETTKGCKYCFMNSGEGDKPLTTTVKGSTNGLEIMDIOQDEYLRPIWGTEETFEAGVK	245		
QY	239	VOIHQOEPRITDGLGLGVSFGYTFVSCQOQOQSLTPPPMDCCSASLNPVYEEPPSP	298		
DB	246	VOIHQOSEPRITDGLGFGVAPGQFVVAQEOERLYLPLPPWGCERSSEMGDLF-----	298		
QY	299	LSPPSPSPPTLMLGCRACETRVYARCGGRMYMPDVPVCSPOQKNCANPAIDAI	358		
DB	299	-----FPVYSITRACRIDCETRIYVENCNRMVHMPDAPFCPTPQKBECAEPALGLI	350		
QY	359	LKKDS--CACPNPCASTRYAKELSMWRIPSRAAARFLARKLRSEAYIAENVALDIFE	416		
DB	351	AEKDSNYICLRPCNLTTRYKELSMWKIPSKTSYAKYLEKFKMSKSEYISENLTVDIFE	410		
QY	417	ALNTEYEQKAYESELGDTGGOMGLFTGASLTILETIDYLCDFPDKVLGFWMNQ	476		
DB	411	ALNTEYIEQKAYEVAALGDTGGOMGLFTGASLTILETIDYLYELIKELLDLGKE	470		
QY	477	HSQRHSSTNLQEGSGSHRTQVPH	500		
DB	471	EGSHDENKSTCDTPMNHSETISH	494		
RESULT 2					
BNAL_HUMAN					
ID	BNAL_HUMAN	STANDARD:	PRT:	512 AA.	
AC	Q16515; Q13553;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Amiloride-sensitive brain sodium channel BNAC1 (Amiloride-sensitive cation channel neuronal 1) (BNAC1) (degenerin channel MDEG).				
GN	ACCN1 OR BNAC1 OR ACCN OR MDEG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RC	MEDLINE=96209957; PubMed=8631835;				
RA	Waldman R., Champigny G., Voilley N., Lauritzen I., Lazdunski M.;				
RT	"The mammalian degenerin MDEG, an amiloride-sensitive cation channel				
RT	activated by mutations causing neurodegeneration in Caenorhabditis				
RT	elegans.";				
RL	J. Biol. Chem. 271:10433-10436(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RC	MEDLINE=96215169; PubMed=8626462;				
RA	Price M.P., Snyder P.M., Welsh M.J.;				

```
RT "Cloning and expression of a novel human brain Na+ channel.";
RL J. Biol. Chem. 271:7879-7882(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Frontal cortex;
RX MEDLINE=97188490; PubMed=9037075; Garcia-Anoveros J., Derfler B.H., Neville-Golden J., Hyman B.T., Corey D.P.;
RA *Bnac1 and Bnac2 constitute a new family of human neuronal sodium channels related to degenerins and epithelial sodium channels.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:1459-1464(1997).
CC CC -I- FUNCTION: NON-VOLTAGE-GATED ANILORIDE-SENSITIVE CATION CHANNEL PERMEABLE FOR SODIUM, POTASSIUM AND LITHIUM.
CC CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -I- TISSUE SPECIFICITY: BRAIN AND SPINAL COD.
CC CC -I SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS FAMILY.
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DR EMBL, U53212; AAC50498..1;
DR EMBL, U50352; AAC50432..1;
DR EMBL, U57352; AAB49182..1;
DR MIM, 601784;
DR InterPro; IPR001873; ASC.
DR Pfam; PF00858; ASC; 1.
DR ProSite; PS01206; ASC; 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 58 POTENTIAL.
FT DOMAIN 59 427 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 428 448 POTENTIAL.
FT DOMAIN 449 512 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 362 365 N-LINKED GLCNAG. . . ) (POTENTIAL).
FT CARBOHYD 395 392 N-LINKED GLCNAAC. . . ) (POTENTIAL).
FT COMPLECT 495 495 T -> A (IN REF. 2).
SO SEQUENCE 512 AA; 57709 MW; 7c95BDB3ZEFf2814 Chk64;

Query Match 47.9%; Score 1365; DB 1; Length 512;
Best Local Similarity 50.6%; Pred. No. 1.6e-102;
Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;
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DR EMBL: U78181; AAB48981.1; -.  
 DR MIM: 602866; -.  
 DR InterPro: IPR001873; ASC.  
 DR Pfam: PF00858; ASC; 2.  
 DR PROSITE: PS01206; ASC; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 45 65 POTENTIAL.  
 FT DOMAIN 66 476 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 477 497 POTENTIAL.  
 FT DOMAIN 498 574 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 434 479 MISSING (IN ISOCFORM 2).  
 SQ SEQUENCE 574 AA; 64841 MW; 8A981AB81488C3A CRC64;  
 Query Match 45.5%; Score 1298; DB 1; Length 574;  
 Best Local Similarity 45.7%; Pred. No. 4.7e-97;  
 Matches 258; Conservative 78; Mismatches 129; Indels 100; Gaps 9;  
 QY 13 QPDSIVFASNCMHGIFGFGPSLIRGGMMAAVVLSVATFLVQARVRYRFRFH 72  
 DB 14 QPVSQAFSSSTLHGIAHFEYERLSLKRALALCFGLAVLLCVCTERVQYRHYHH 73  
 QY 73 QTAIDRESHRVPAVTLICNINPLRRSRLLTPDLHWAGS--ALLG----- 116  
 DB 74 VTKLDEVAASQLFPVATLCLNLFNRFQSKNDIVHAGELLALLNNRYEIPDTQMADEK 133  
 QY 117 -LDPAAHAFLRALGRPPAPGFMSPETDMAOLVARGHSLDDMLDCFRQPCGPEH 175  
 DB 134 QLEILLDDKNFRS-----FKPR-FMREFYDRAGHDIDMLSCHFGEVCSAED 183  
 QY 176 FTFITFMGKCYFENGADCAELTTTRGGMGNDIMLDVQOEVLVPRVNDENFEV 235  
 DB 184 EKVFTRFKCYTFNNGRDRPRLKTKMDGTGNGLEIMLDQDEYLPVWGETDETSFEA 243  
 QY 236 GIRVQIHSGEPPRIIDGLGVSPGYQTFVSCQQOQLSFLPPWGCSSASLNPTEPEP 295  
 DB 244 GIKVQIHSDDEPFIQDLGFGVAFQTFVACQEQRLIYLPWPWGCKAVTMSDIDFDP 303  
 QY 296 SDPLGSPSPSPPTLMLGCRCLACETRYVARKGCGRMVYPCGVPVCSPOQYRNCAPAI 335  
 DB 304 S-----YSITACRIDCETRYLVENCNCRVHHPGAPCYCTPEQYECADPAL 350  
 QY 356 DAILRKDS--CACPNPCASTRYAKETSMVRIPSRAARFLARKLNSEAYIAENVLALDI 413  
 DB 351 DFLVEYDQECYCEMPCNLTRYKELSMVKIPKASAKYLAKKFNKSEQYIGENIYLDI 410  
 QY 414 FFEALNYETVEOKKAYEMSEL----- 434  
 DB 411 FFEVLNYETIEOKKAYEIGLGLLELMTVPFSCGHGVAPYHPKAGCSLLSHEGPPQR 470  
 QY 435 -----LGDIGGOMGLFGASLITLLELDYLCEVFRKVLGYFMNRRQSHSTNLL 487  
 DB 471 PEPPCCCLDDIGOMGLFGASLITLLELDYAVEYIKKHLK---RKGCKQEARSSA 526  
 QY 488 QEGLSHRTQVPHLSLGRPPPTPPC 512  
 DB 527 DKGVA-----LSLDVYKRHNPC 543  
 RESULT 5  
 SCAA\_MOUSE STANDARD: PRT: 699 AA.  
 AC 061180: 09WU37;  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 16-OCT-2001 (rel. 40, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE Amloride-sensitive sodium channel alpha-subunit (Epithelial Na+ channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel 1 alpha subunit) (SCN5A) (Alpha NaCh).  
 GN SCN5A.

OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Kidney;  
 RX MEDLINE=99345762; PubMed=10409305;  
 RA Ahn Y.J., Brooker D.R., Kosari F., Harte B.J., Li J., Mackler S.A., Kleyman T.R., [et al.]  
 RT "Cloning and functional expression of the mouse epithelial sodium channel."  
 RL Am. J. Physiol. 277:F121-F129(1999).  
 RN [2]  
 RP SEQUENCE OF 445-558 FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Kidney;  
 RX MEDLINE=97428085; PubMed=9284273;  
 RA Dagenais A., Kothary R., Berthiaume Y.;  
 RT "The alpha subunit of the epithelial sodium channel in the mouse: developmental regulation of its expression".  
 RL Pediatr. Res. 42:327-334(1997).  
 CC - FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY) THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS. ALSO PLAYS A ROLE IN TASTE PERCEPTION.  
 CC - SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.  
 CC - TISSUE SPECIFICITY: INTEGRAL MEMBRANE PROTEIN.  
 CC - LOW EXPRESSION IN LIVER.  
 CC - SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS FAMILY.  
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 CC -----  
 DR EMBL: AF112185; AAD21244.1; -.  
 DR EMBL: U52006; AAG97412.1; -.  
 DR MGI: 101782; Scnla.  
 DR InterPro: IPR001873; ASC.  
 DR Pfam: PF00858; ASC; 1.  
 DR PRINTS: PRO1078; AMINACHANNEL.  
 DR PROSITE: PS01206; ASC; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein;  
 FT DOMAIN 1 110 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 111 131 POTENTIAL.  
 FT DOMAIN 132 589 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 590 610 POTENTIAL.  
 FT DOMAIN 611 698 POTENTIAL.  
 FT DOMAIN 68 71 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 71 226 POLY-GLU.  
 FT CARBOHYD 190 190 POLY-PRO.  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 445 445 H -> R (IN REF. 2).  
 FT CONFLICT 555 555 FKE -> YKH (IN REF. 2).  
 SQ SEQUENCE 699 AA; 78893 MW; 5B083BB8769B017A CRC64;  
 Query Match 14.7%; Score 420.5; DB 1; Length 699;  
 Best Local Similarity 23.5%; Pred. No. 3.3e-26;  
 Matches 152; Conservative 91; Mismatches 231; Indels 173; Gaps 25;  
 QY 6 GPBEAR-ROPSD-----IVFASNCMHGIFGFGPSLIRGGMMAAV 49

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DB 57 GPEPSPRPQTEEEALIEFHRSYRELFOFCNNTTIGHAIRLVCCKHNMKTAFAVLW 116
OY 50 VLSVATFLYQVARNRYRYEFHHQALD--ERESHRLVFPAYVLCTINPLRRSL----- 102
DB 117 LCTFGMMYQOFALLFEY--FSYPSLINTLNLSKDLVPAVVCCTINRYTETIKEDLEE 174
OY 103 -----TPNDLHMWAGSA-----LLGLDPAEHAFLRALGPRPPGPMPS 141
DB 175 LDRITQTLFDLYKYNSTTRQAGRRRSTRDLRGALP--HP--LQRLTRPP--PPNPARS 229
OY 142 -----PTFD-----MAOLY----- 150
DB 230 ARSASSVBDNNQVDRKDKIGFOLCNOUKSCDFQYSSGVDAVREMYRHYINILSR 289
OY 151 -----ARAGHSLDMLDCRFGRGCPGNFTITTRM--GKTYTNSGADGELLTTR 203
DB 290 LDPSTALBEEALSFETFCRFNOAPCNOANYSQFHHPMYGCNCTENN--KNSNLMMSSM 348
OY 204 GKGNGGLDMLDVQOEYLPVWMDNETPREVEGIRVOIHSEEPPIIDQLGLVSPGYOT 263
DB 349 PGVNNGLSLTRTEQNDPL-----LSTVGARVWVHGQDPAFMDGCFVVRGVEET 402
OY 264 FVSCQOQOISFLPPWGDSSASLNPYEPSPDPLGSPSPSPPYTLMGCRACETRY 323
DB 403 SISMRKREALDSLGNGVGDCT-----ENGSDVPVKNLYPS--KYTQCVCHSCQEN 451
OY 324 VARKCCGRMYMPGDVPCVSPQOYKNC-----AHPADAILRKDSCA---CPNP 369
DB 452 MIRKCCCAFIYFP-----KPKGVFECDYLKQSSMGVCYKYLQAAFSLSLSCFSCRKRP 505
OY 370 CASTRAKELSMVRIPSRBAARFLARKLNSEAYIEN-----VLADIEPEALNYEVEQ 425
DB 506 CSTNTKLSAGYSRMPSVKSQDWIFEMLSLQNNYTTNNKRNKGAKNIFEKELNYTNS 565
OY 426 KRAVENSELLDIGOMGLFPGASLTLEILIDYCEV-----FRDVLGFWN 474
DB 566 SPSTVWVSLNSLQMSQMSLWFGSSVLSVEMALIFDLVITLIMLHRRSR-----YWS 621
OY 475 RQHSQR-----HSTNLIQEGISHRTOVPHLSLGRPPPTPCAVT 515
DB 622 PGKAGARGAREVASTPASSPSPRCPTSPPP--SLPQOGTTPLALT 667

RESULT 6
FANA_HELAS
ID FANA_HELAS STANDARD; PRT; 625 AA.
AC 025011;
DR 01-NOV-1997 (rel. 35, Created)
DR 01-NOV-1997 (rel. 35, last sequence update)
DR 15-JUL-1998 (rel. 36, last annotation update)
DE FMRFamide-activated amiloride-sensitive sodium channel (FANACH).
OS Helix aspersa (Brown garden snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Helicacea; Helicidae; Helix.
OX NCBI_TaxID=6535;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nerve;
RX MEDLINE=96107314; PubMed=7501021;
RA Lindegglia E., Champigny G., Lazdunski M., Barbry P.;
RT "Cloning of the amiloride-sensitive FMRFamide peptide-gated sodium
channel".
RL Nature 378:730-733(1995).
CC -!- FUNCTION: FMRFAMIDE-GATED IONOTROPIC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: MUSCLE AND NERVOUS TISSUE.
CC -!- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X92113; CAA63084.1; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PROSITE: PS01206; ASC; 1.
KW Ionic channel; Transmembrane; Glycoprotein.
FT DOMAIN 1 67 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 68 89 POTENTIAL.
FT DOMAIN 90 536 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 537 557 POTENTIAL.
FT DOMAIN 558 625 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 578 581 POLY ASN.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 625 AA; 71350 MW; CF2E7409CA5B82A6 CRC64;

Query Match 14.7%; Score 419; DB 1; Length 625;
Best Local Similarity 22.2%; Pred. No. 3.8e-26;
Matches 136; Conservative 99; Mismatches 191; Indels 186; Gaps 20;

OY 17 IRVAFASNCNMGHGVFPGLSLRGRGMAAAVLVAVAFELYQVARNRYRYEFHHQAL 76
DB 43 IAEGLSSNMHGLAKITYTSD--TKRYVAMLLYIAGTATATDLSLVKRYLOFOVELS 101
OY 77 DERESHRLVFPAYVLCTINP-----LRR--SRTPNDLHMWAGSALLGLDPAEHAFLRA 128
DB 102 EIKDSMVQYPSVINCINIEPISLRTIRMYFNESONLITWL--RFLQKRFQDSEFMS 159
OY 129 LGRPPAPRGMPPTF--DMAQLYARAGSLDMLDCRGRGCPGNFTTFT--RMCK 185
DB 160 I-----RAFENIGDQAKKLSHMLEMHCNRNRELCHVSNSTFDCGYEN 207
OY 186 CYTFNSGADGAEILTTTRGGMGNDLMDVQOEYLP-----VWRDNEETPFVEGIRVOI 241
DB 208 CFTFNSG-----QRLQMHATGPENGSLIFSEKDDPLPGYGYVYNNNDNLTLSAGRVVY 263
OY 242 HSGEPEPIIDQLGVSPGYQTFFVSCQOQOISFLPPWGDSSASLN--PNYEPSPDPL 299
DB 264 HAPGSMPSVVDHGIDIDIPGYSVGLKALIDHTRLPYPGNCTMDMLNGIKQYK----- 316
OY 300 GSPSPSPSPRYTLMGCRACETRYVARKCGGRMYMPGDV----- 340
DB 317 -----YTFPACLDQKRLIIRQCGCKSSALP--EVPSTNATFCGYIKDQELNRN 365
OY 341 -----VCSPOQYKNCARPAIDAILRKD-----SCACPNCPCASTR 374
DB 366 HSNEDHNSQEDBAFIPTPLACBERQKN-----LMDRYELSCGCGPCGSETS 416
OY 375 YAKELSMVRIP-----SRAARFLARKLNSEAYIA----- 405
DB 417 YLKSVSLSYPLBIFYQLSAVERFKQERQAGQNHFMKATAYELEKLANHRSQHLARDSH 476
OY 406 -----ENVLADLIEFFALNTEYBQKAYKMSLLDIDIG 440
DB 477 MDDLKSYSLSEKAKKASDLIRQMLNLNITLEDLSVEYRQLPAGVALDLPADIG 536
OY 441 QMGFLFASLTLEILIDYCEVFRDVLGVPNNRQ-----HSQRHS 482
DB 537 TLGLMGISVITLMELIELYI-----RLTGLVENSEGLPRGTYVNNNGNSNNHQ--ST 590
OY 483 STNLIQEGLSH 494
DB 591 SQHQLVNGYMDH 602
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RESULT 7
SCB2_XENLA          STANDARD:          PRT:          646 AA.
ID   SCB2_XENLA          STANDARD:          PRT:          646 AA.
AC   O13262:
DE   15-JUL-1998 (Rel. 36, Created)
DE   15-JUL-1998 (Rel. 36, Last sequence update)
DE   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Amiloride-sensitive sodium channel beta-2 subunit (Epithelial Na(+)
DE   channel beta-2 subunit) (Beta-2 ENAC) (Nonvoltage-gated sodium channel
DE   1 beta-2 subunit) (SCNBE2) (Beta-2 NACH).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Puoti A., May A., Rosslar B.C., Horisberger J.D.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC   FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC   INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
CC   OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC   THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC   REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC   ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC   -1- SUBUNIT: HETEROTRIMER OF AN ALPHA, BETA AND GAMMA SUBUNIT, A DELTA
CC   SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC   -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC   FAMILY.
CC   -----
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL: Y12000; CAA72729.1; -.
DR   InterPro: IPR001873; ASC.
DR   Pfam: PF00858; ASC.1.
DR   PRINTS: PRO1078; AMINACHANNEL.
DR   KIR PROSITE: PS01206; ASC.1.
KW   Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT   DOMAIN 1             1      56      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM 57          77          POTENTIAL.
FT   DOMAIN 2             78          552      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM 553          572          POTENTIAL.
FT   DOMAIN 3             573          646      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD 146          146          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 151          151          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 195          195          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 217          217          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 225          225          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 278          278          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 383          383          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 397          397          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 429          429          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD 468          468          N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE 646 AA; 74112 MW; 30126C9B864BFB0 CRC64;
Query Match 14.8%; Score 417; DB 1; Length 646;
Best Local Similarity 22.8%; Pred. No. 5.8e-26;
Matches 142; Conservative 93; Mismatches 227; Indels 160; Gaps 23;
QY 20 FASNCSMHGLHVGPGSLDRGMAAAYLVSAATFLYOVAERYRREFHQTALDER 79
DB 35 FCDMTNFTGPRRIKES--PKRWMMFLTLVPAFLVFMQGLLITLVLSGVSYSL-SI 91
OY 80 ESHRLVPAATVLCNINPLRSRLTP--NDL-HMAGSAL----- 114
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DB 92 GPKTMEFPATVCTNPNKYKSRKPLDLDELVAATLDRIOYSSOTOANFTYNNTRON 151
OY 115 LGIDPA--EHAAPFLNALGRPAAPGFMSPFEDMAQLYAR----- 152
DB 152 VTLDELALNNHITLVVIDENDPSNP--VIHNIDNSVFTSKNNLLNNSSEDTGYAQRKYV 209
OY 153 -----AGSLDDMLLDCRF 166
DB 210 AMKLCTNNNTQCVYRNFTSGVQALREWYLLQSLIFSNVPLSDRYDMGFKADLLITLCLE 269
OY 167 KQPCGPEFTTIF--TRMGKCTFNSGADGALLTTTGKMGNGIDIMLDVQOQETLYW 225
DB 270 GGQPCSYRNFTIYADYDNCCTIFMGGQEDPMSNAPGAFGLKVLVDLEQDEYLPFL 329
OY 226 RDNEEFPFVGIRVOIHSEEPPIIDGLGVPQYQTFVSCQOQOGLFLPPMGDC--- 282
DB 330 QTT-----AAKRLHQORSFPFYKDLGYAKPFTETSIATLVQLODMEPYSSCTVYN 383
OY 283 -SSASINPVEPEPSDPLGSPSPSPPTLMGCRLACETRYVARKGCR--MYMPGDV 339
DB 384 GSDIPVQNLVEEFNS-----YSIQSCLRSCQYEEWVKCKAHYQYPLPNGS 431
OY 340 PVSQPOQYKN---CAHPAIDALRKDSC--ACPNCASSTRAKELSMYRIPRAARLA 394
DB 432 EYCTNNKHPDWPCYCYGLRDSVAIRENCISLQCPQDPTFRKMWISMDWPSAGAEWIF 491
OY 395 RKLN--RSEAY-IAEN---VLALDFFEALNYEYQKAVEMSELGIDGOMGLFTGA 448
DB 492 HLYSEKXSDVDTYNNRNGIIRLNTYFQEPFNRSISEEATVWVLLNLGSGQFPMWNG 551
OY 449 SLTLLEILDYCE---VFRDKVLCYFNW-ROHSOR-----HSTNL-LQE 489
DB 552 SVLCIEEGEIIIDDMWTIKLWIMINRRORRQAPYADPPYSELVEAHTNPGQH 611
OY 490 GIGSHRTQVPHSLGRPPTP 511
DB 612 DDGNHYTE-----DIPCTTP 626
RESULT 8
SCAB_XENLA          STANDARD:          PRT:          647 AA.
ID   SCAB_XENLA          STANDARD:          PRT:          647 AA.
AC   P51169:
DE   01-OCT-1996 (Rel. 34, Created)
DE   01-OCT-1996 (Rel. 34, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Amiloride-sensitive sodium channel beta-subunit (Epithelial Na+
DE   channel beta subunit) (Beta ENAC) (Nonvoltage-gated sodium channel 1
DE   beta subunit) (SCNEB) (Beta NACH).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Puoti A., May A., Canessa C.M., Horisberger J.D., Schild L.,
RA   Rosslar B.C.;
RL   MEDLINE=9538264; PubMed=7631745;
RL   Am. J. Physiol. 269:C188-C197(1995).
CC   FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC   INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
CC   OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC   THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC   REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC   ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC   -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC   SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (BY
CC   SIMILARITY).
CC   -1- SUBCELLULAR LOCATION: Integral membrane protein.

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CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS  
 CC FAMILY.  
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DR EMBL: U05285; AAA74971.1; -.  
 DR InterPro: IPR001873; ASC.  
 DR Pfam: PF00858; ASC; 1.  
 DR PRINTS: PRO1078; AMINCHANNEL.  
 DR PROSITE: PS01206; ASC; 1.  
 KM Ionic channel; Transmembrane; Ion transport; Glycoprotein.  
 FT DOMAIN 1 56 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 57 77 POTENTIAL.  
 FT DOMAIN 78 553 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 554 573 POTENTIAL.  
 FT DOMAIN 574 647 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 504 504 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 647 AA; 73976 MW; 3A85366BF0E3F16 CRC64;

Query Match 14.6%; Score 415.5; DB 1; Length 647;  
 Best Local Similarity 22.0%; Pred. No. 7.6e-26;  
 Matches 135; Conservative 92; Mismatches 231; Indels 155; Gaps 19;

QY 20 FAANCSMHGAGHVPFGSGSLRKGMAAAVSVATFLVQVAERVRYRFFHQTLADER 79  
 DB 35 FCDNTYHGGKRLIKGG--PKRRVMFILLVFAGLVFMQGVLLITYLSYGVSVL-SI 91  
 QY 80 ESHRLVPAVATLCNINPLRSRLTP-----NDHMWAGSAL----- 114  
 DB 92 GFKTMEFPVATLCNANPEKYSRKPLKEDEL--VATALDRIQFSQNGNFTNNQT 149  
 QY 115 ---LGLDPA--EHAFLRALGRPPAPGFWPSPFPMAQLYAR----- 152  
 DB 150 RQWVTLDPALMNIHPLVVIDETPRNP--IIHIFPNNAVYSKNSIRNSSEDQTSYQR 207  
 QY 153 -----AGHSLDMLD 163  
 DB 208 YKVAFLCTNNNTQCYVRNFTSGVALREWYLLQLSSIFSNVPLSGRIDGFAEDLLLT 267  
 QY 164 CREFGQPCGEPENTTIF--TRMGKCYFNSGADAEILLTTRGGMGLDMLVQOEEYL 222  
 DB 268 CLEGGQPCYRNTHIYDADYGCYIFNMGQEBENTMSSNPADGKLIVLDEGEYL 327  
 QY 223 PWRNDNEETPEFVEYGRVQHSQEEPIIDOLGIVSPGYOTVFSQOOQLSFLLPPWGD 282  
 DB 328 PFLQTT-----AAARLIHQQRSPFVKDLGITAMPGETSISLVLDQEHMEARVYSSC 381  
 QY 283 SSKSLNPNTPEPESD--PLSPSPSPSPPTLMGCRACETRYVARKCGCR--WVYMPGDV 339  
 DB 382 T-----VNGSDIPVONLVAEFNYSYSIOSCLRSQYOEENVKCKCAHYQYPPNGS 432  
 QY 340 PWCSPQOYRN---CAHPAIDAILRKDSC--ACFPNCASTRYAKELSMVRISPAARFLA 394  
 DB 433 EYCTNNKHDPDWVCYSLSDSVAIRENCISLQOQPCNDHNYKKNVISMADMPSGAGADWIF 492  
 QY 395 RKLN---RSEAYIAEN---VLALDIFFEALNFTYVQKRAYEKSELLGDIGOMGLFIGA 448

DB 493 HVLSEKDDSSNITVNRNGRIYLVITFOERNYSISESTNWWLSNLGGQGFWMGG 552  
 QY 449 SLATLLEILDYLCFPRDKYLYGF-WNRQHSQRHSSTNLLQEGLSHRTQVPHLSGPRP 507  
 DB 553 VSLCIIIEFGELIIDCMWITLTKFLAMSRNNRRQRK-----PQY 591  
 QY 508 PTPPCAATYTKTLA 520  
 DB 592 SDPEPTVSELVEA 604

RESULT 9  
 SCAA\_RAT  
 ID SCAA\_RAT STANDARD; PRT; 698 AA.  
 AC P37089; Q64593;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Amiloride-sensitive sodium channel alpha-subunit (Epithelial Na+  
 DE channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel  
 DE 1 alpha subunit) (SCN5A) (Alpha NaCh).  
 GN SCN5A OR RENAC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RX STRAIN=MISTAR; TISSUE=Distal colon;  
 RX MEDLINE=93170495; PubMed=8382172;  
 RA Lingueglia E., Volley N., Waldmann R., Lazdunski M., Barbry P.;  
 RT "Expression cloning of an epithelial amiloride-sensitive Na+ channel.  
 RT A new channel type with homologies to Caenorhabditis elegans  
 RT degenerins.";  
 RT FEBS Lett. 318:95-99(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Colon epithelium;  
 RX MEDLINE=93156815; PubMed=8381523;  
 RA Canessa C.M., Horisberger J.D., Rossier B.C.;  
 RT "Epithelial sodium channel related to proteins involved in  
 RT neurodegeneration.";  
 RL Nature 361:467-470(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=Mistar Kyoto, AND SHRSRP; TISSUE=Kidney;  
 RX MEDLINE=97191134; PubMed=9039092;  
 RA Kreutz R., Strub B., Rubattu S., Hubner N., Szpirer J., Szpirer C.,  
 RA Ganten D., Lindpaintner K.;  
 RT "Role of the alpha-, beta-, and gamma-subunits of epithelial sodium  
 RT channel in a model of polygenic hypertension.";  
 RL Hypertension 29:131-136(1997).  
 RN [4]  
 RP TOPOLOGY, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=95014183; PubMed=7929098;  
 RA Snyder P.M., McDonald F.J., Stokes J.B., Welsh M.J.;  
 RT "Membrane topology of the amiloride-sensitive epithelial sodium  
 RT channel.";  
 RL J. Biol. Chem. 269:24379-24383(1994).  
 RN [5]  
 RP TOPOLOGY.  
 RX MEDLINE=94230383; PubMed=8175716;  
 RA Renard S., Lingueglia E., Volley N., Lazdunski M., Barbry P.;  
 RT "Biochemical analysis of the membrane topology of the amiloride-  
 RT sensitive Na+ channel.";  
 RL J. Biol. Chem. 269:12981-12986(1994).  
 RN [6]  
 RP MUTAGENESIS OF SER-589 AND SER-593.  
 RX MEDLINE=95263507; PubMed=7744818;  
 RA Waldmann R., Champigny G., Lazdunski M.;  
 RT "Functional degenerate-in-containing chimeras identify residues essential  
 RT for amiloride-sensitive Na+ channel function.";

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RL J. Biol. Chem. 270:11735-11737(1995).
CC - FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIANE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC - SUBUNIT: HETEROPTRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X70521; CAA49916.1; ALT_INTIT.
DR EMBL: X70457; CAA49905.1; -.
DR EMBL: U54699; AAB61156.1; -.
DR EMBL: U54700; AAB61157.1; -.
DR PIR: S29499; S29499.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 1.
DR PRINTS: PRO1078; AMINCHANNEL.
DR PROSITE: PS01206; ASC. 1.
KW IONIC channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 110 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 111 131 POTENTIAL.
FT TRANSMEM 132 589 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 590 630 POTENTIAL.
FT DOMAIN 611 698 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .).
FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .).
FT MUTAGEN 588 588 S->I: CHANGES FUNCTION OF THE CHANNEL
INCLUDING CONDUCTANCE, GATING,
SELECTIVITY AND VOLTAGE DEPENDENCE.
FT MUTAGEN 592 592 S->T: CHANGES FUNCTION OF THE CHANNEL
INCLUDING CONDUCTANCE, GATING,
SELECTIVITY AND VOLTAGE DEPENDENCE.
FT CONFLICT 598 599 EL -> DV (IN REF. 2).
FT SEQUENCE 698 AA; 78887 MW; B0CF7C15C3CE9763 CRC64;
SQ
Query Match 14.5%; Score 414.5; DB 1; Length 698;
Best Local Similarity 22.9%; Pred. No. 1e-25;
Matches 147; Conservative 97; Mismatches 236; Indels 161; Gaps 21;
QY 6 GPE-EAROPSD-----IRVFASNCNMHGLGVFGPGSLSRGMMAAV 49
DB 57 GPEPSAPROPTEEDEALIEFHSRYRELFOFCNNNTTHGAILRVCSEKHNMKAFNA--- 113
QY 50 VLSVAFLVQVAERVRKYREF-HHQTALD-ERSHRLVFAVYLCINPLRARRL----- 102
DB 114 VLMICFEGMYWQFALLFEFEYLSYPVSLNINLNSDKLVFAVYVCTLNPVRYTEIEELE 173
QY 103 -----FPNDLHMAGSALGLDPAEHAFLALGPRPAPGPMSPPTDMQOLYARAG 154
DB 174 ELDRITEQTLFDLYKYNSSITRQAGARRRSSRLDGAFFPDLRLKRPPTPPYSGRTARRSG 233
QY 155 HS----- 156
DB 234 SSSSVRONNPVDRKDKMIGFQLCNQNKSDCFYQTYSSGVDAVREMYRFHYINILSLSDT 293
QY 157 -----LDDMLDCRFRCQPCGPEPNTTIFTRM-GKCTTFPSGADGAEALLTTTRGGMG 207

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DB 294 SPALBEALGNFIETCRFNOAPCNOANYSKREHPWYGCYTFEND-KNNSNLMSGMPGVN 352
QY 208 NGLDMLDVOQEEYLPVRNDNEPFEVGIRYQIHSOEPPLIDGLGVSFGYQTEVSC 267
DB 353 NGLSLTLRTEQNDPFLP-----LSTVGARVMVGDQEPAPMDGNGNLRPGVETISIM 406
QY 268 QOQQLSFPPPGDSSASLANPNEPSPDLPSPSPSPSPPTYLMLGRCLACETRYARK 327
DB 407 RKEALDSLGNVDCDT-----ENGSDVPYKNLYPS---KYTOQVCHSCFOENMIKK 455
QY 328 CCCRMVY--MPQDVYVCSPOQ-----YKNCAIPALDAILRKSC--ACQNPASIRY 375
DB 456 CCCAVTFPPKPGVEFCYRKQSSWGYCYKLGAFSLDSL---GCFSKCRKPCSVYNT 511
QY 376 AKELSWVRIPSRRAARFLARKLNRESEAYIAEN---VLALDIFFEALNYETVEOKAYEM 431
DB 512 KLSAGYSRPFYSKSDQWIFEMLSLONNTTINKRNGVAKLNFFELMYKTNSESPVTM 571
QY 432 SELLDIGQMGFLTGASLTLEILDYLCFY-----PDKVLYGFYRNQHSOR 480
DB 572 VALLSNLGSQMSLWFGSSVLYVEMAELIFDLVITLLMLLRFRSR---YWSPRGAR 627
QY 481 -----HSTNLLQGLSGHRTQVPHLSLGPAPPTPCAVT 515
DB 628 GAREVASTPASSPSPSRFCPHPTSPPP-SLPQOGMTPLALT 667

RESULT 10
SCAA_HUMAN STANDARD; PRT; 669 AA.
ID SCAA_HUMAN
AC P37088;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amiloride-sensitive sodium channel alpha-subunit (Epithelial Na+
DE channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel
DE 1 alpha subunit) (SCN5A) (Alpha NaCh).
GN SCN5A OR SCNN1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94105144; PubMed=8278374;
RA Volley N., Languegla E., Champigny G., Mattei M.-G., Waldmann R.,
RA Lazdunski M., Barbry P.;
RT "The lung amiloride-sensitive Na+ channel: biophysical properties,
RT pharmacology, ontogenesis, and molecular cloning.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:247-251(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94295729; PubMed=8023962;
RA McDonald F.J., Snyder P.M., McCray P.B., Welsh M.J.;
RT "Cloning, expression, and tissue distribution of a human amiloride-
RT sensitive Na+ channel.";
RL Am. J. Physiol. 266:L728-L734(1994).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=98316780; PubMed=9654208;
RA Ludwig M., Boikenius U., Wickett L., Marynen P., Bldingmaier F.;
RT "Structural organisation of the gene encoding the alpha subunit of
RT the human amiloride-sensitive epithelial sodium channel.";
RL Hum. Genet. 102:576-581(1998).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=99374783; PubMed=10447117;
RA Chow Y.H., Wang Y., Plumb J., O'Brodoovich H., Hu J.;
RT "Hormonal regulation and genomic organization of the human amiloride-
RT sensitive epithelial sodium channel alpha subunit gene.";
RL Pediatr. Res. 46:208-214(1999).

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CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DISEASE: DEFECTS IN SCNNIA ARE ONE OF THE CAUSES OF
CC PSEUDOHYPONATREMISM TYPE 1 (PHA1), A RARE SALT WASTING DISEASE
CC CHARACTERIZED BY AN OFTEN FULMINANT PRESENTATION IN THE NEONATAL
CC PERIOD WITH DEHYDRATION, HYPONATRAEMIA, HYPERKALAEMIA, METABOLIC
CC ACIDOSIS, FAILURE TO THRIVE AND WEIGHT LOSS.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
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CC -----
DR EMBL: X76180; CAA53773.1; -
DR EMBL: I29007; AAA21813.1; -
DR EMBL: Z82978; CAB07505.1; -
DR EMBL: Z82979; CAB07505.1; JOINED.
DR EMBL: Z82980; CAB07505.1; JOINED.
DR EMBL: Z82981; CAB07505.1; JOINED.
DR EMBL: AF060913; AAD28355.1; -
DR EMBL: AF060910; AAD28355.1; JOINED.
DR EMBL: AF060911; AAD28355.1; JOINED.
DR EMBL: AF060912; AAD28355.1; JOINED.
DR MIM: 600228; -
DR MIM: 177735; -
DR MIM: 264350; -
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 1
DR PRINTS: PRO1078; AMINCHANNEL.
DR PROSITE: PS01206; ASC. 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 POTENTIAL.
FT DOMAIN 107 562 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 563 583 POTENTIAL.
FT DOMAIN 584 669 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 669 AA; 75703 MW; 2CCF342E7DF32E72 CRC64;

Query Match 14.3%; Score 407.5; DB 1; Length 669;
Best local similarity 22.2%; Pred. No. 3.5e-25;
Matches 152; Conservative 96; Mismatches 225; Indels 211; Gaps 26;

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DB 201 RRAASVASSLRDNNPQYDWMKDWKIGFQLCNQNKSDECFYOTSSGVDVAREMYRPHYINIL 260
QY 154 -----GHSDDMLDCCRFRGPGCPENFTTFTSM-GKCTYFNGAGACELTT 201
DB 261 SRUPETLPSEETPLGFIACRNOVSCQANYSRHHADMYGNCYTFND-KNNSNLNMS 319
QY 202 TRGGMGLDMLDVOOEFLPVARNDEETPEFVGIRVOIHSOEEPIIDOLGIGVSGY 261
DB 320 SMGCIINGSLMLRAEONDFIPL-----ISTYGARVYVHGODEPFFMDGGFNLRPV 373
QY 262 QTFVSCQOQOLSFPPWPWGSSASLNPNYEPSPD-PLGSPSPSPPTLMGCRACE 320
DB 374 ETSISMKEKELDLRGDYGQOTK-----NSDVPVENLVP-----KTYQVCISHC 421
QY 321 TRYVARKCGCRMYMPEDVYVCSPOQYKNCAPDAIDILKDS----- 363
DB 422 QESMKICGCAIIFYP-----RPQNEYCDY-----RKHSWGVCYKLOVDFSSDH 468
QY 364 -----CACPNPCASRYAKELSMVRIPRRAARFLARKLNSEAYIAEN-----VLADIFF 415
DB 469 LGCTTKRKRCPSVTSTYLSAGYSRMPSVTSEWVFQMLSHONNTYVNNKRYAKVWIF 528
QY 416 EALNYETVEQKAYEMSELLDGGOMGFLTGASLTILTEILDYCEV-----F 464
DB 529 KELNYKTNSESPSVTVVTLNLGSOQSLMFGSSVLSVEAEVLFIDLVIIMLLRRF 588
QY 465 RDKVLGTFNRRHQSQRHS--TNLDGGLSHRQVYH--LSIGRPPPPPCAVTK--- 516
DB 589 RSR---YWSPPGRGRGAQEVASTLASSPPSH--FCBPHMSSLISOPAPAPALTRAPP 642
QY 517 -----TLASHRTCYL 527
DB 643 AYATLGPSPSGSAGASSSTCPL 666

RESULT 11
SCAA_BOVIN
ID SCAA_BOVIN STANDARD; PRT; 650 AA.
AC P55270; O02851.
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Amiloride-sensitive sodium channel alpha-subunit (Epithelial Na+
DE channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel
DE 1 alpha subunit) (SCNNA) (Alpha NaCh).
GN SCNNA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RX MEDLINE=96032429; Pubmed=7573394;
RA Fuller C.M., Awayda M.S., Arrate M.P., Bradford A.L., Morris R.G.,
RA Genessa C.M., Rossier B.C., Benos D.J.;
RT "Cloning of a bovine renal epithelial Na+ channel subunit.";
RL Am. J. Physiol. 269:C641-C654(1995).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Benos D.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS

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CC      FAMILY.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U14944; AAB48988.1; -.
DR      InterPro: IPR001873; ASC.
DR      Pfam: PF00858; ASC. 1.
DR      PRINTS: PR01078; AMINACHANNEL.
DR      PROSITE: PS01206; ASC. 1.
KW      Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT      DOMAIN 1 65 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 66 86 POTENTIAL.
FT      DOMAIN 87 543 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 544 564 POTENTIAL.
FT      DOMAIN 565 650 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 650 AA; 73793 MW; C17CB6C1ECB60B9A CnC64;
Query Match 14.0%; Score 400; DB 1; Length 650;
Best Local Similarity 21.8%; Pred. No. 1.4e-24;
Matches 145; Conservative 96; Mismatches 226; Indels 198; Gaps 25;

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Oy      471 YFNRHOSRHSSTNLLDGLGSHRTQ-----VPHLS-LGPRPPPTPCAVT 515
Db      573 -YWS-----PGRGKGTOEVASTRPASLPSSFCPHAFSSPPDP--AIs 615
Oy      516 KTLA 520
Db      616 PALSA 620

RESULT 12
SCAG_RAT
ID SCAG_RAT STANDARD: PRT: 650 AA.
AC P37091.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amloride-sensitive sodium channel gamma-subunit (Epithelial Na+
DE channel gamma subunit) (Gamma ENaC) (Nonvoltage-gated sodium channel
DE 1 gamma subunit) (SCN9G) (Gamma NaCh).
DE SCN9G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN NM
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Distal colon epithelium;
RX MEDLINE=94150624; Pubmed=8107805;
RA Ganessa C.M., Schild L., Bell G., Thorens B., Gautschi I.,
RA Horstberger J.D., Rossier B.C.;
RT "Amloride-sensitive epithelial Na+ channel is made of three
RL Nature 367:463-467(1994).
RN RL
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Distal colon;
RX MEDLINE=94245676; Pubmed=8188647;
RA Linguella R., Renard S., Waldmann R., Volley N., Champigny G.,
RA Plass H., Lazdunski M., Barbry P.;
RT "different homologous subunits of the amloride-sensitive Na+ channel
RL J. Biol. Chem. 269:13736-13739(1994).
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Distal colon, and kidney;
RX MEDLINE=97191134; Pubmed=9039092;
RA Kreutz R., Struk B., Rubattu S., Hubner N., Szpirer J.,
RA Szpirer C., Ganten D., Lindpaintner K.;
RT "Role of the alpha-, beta-, and gamma-subunits of epithelial sodium
RL channel in a model of polygenic hypertension."
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC INHIBITED BY THE DIURETIC AMLORID. MEDATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LONG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMLORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X77933; CAA54905.1; -.
DR      EMBL: X78034; CAA54964.1; -.

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DR EMBL: U37539; AAB58459.1; -.
DR EMBL: U37540; AAB58460.1; -.
DR PIR: S41160; S41160.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 1.
DR PRINTS: PRO1078; AMINACHANNEL.
DR PROSITE: PS01206; ASC. 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 76 POTENTIAL.
FT DOMAIN 77 542 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 543 563 POTENTIAL.
FT DOMAIN 564 650 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 53 53 R -> P (IN REF. 1).
FT CONFLICT 573 573 W -> C (IN REF. 1).
SQ SEQUENCE 650 AA; 74066 MW; 701F9B28B3250D8F CRC64;

Query Match 14.0%; Score 398.5; DB 1; Length 650;
Best Local Similarity 23.2%; Pred. No. 1.8e-24;
Matches 154; Conservative 93; Mismatches 233; Indels 183; Gaps 26;

OY 3 PISGGEARROSDIRVRASNSMGHGVFGPGSLRLRGMAAAVLSVATFLYQAE 62
DB 16 PVRGP-QAPTKIDLMHWCMNTNTGCRRIYVSRG-RLRLIMIAFTLVAALIIWQCL 73
OY 63 RVRVREHHQTALDERESH--RLVEPAVTCINPLRRSR---LTPMDLMWAGSALG 116
DB 74 LV-----ESFYVSVISIVHFOKLDPRVATTCININPYKSAVSDLLTDLDE-TQALLS 127
OY 117 LDPAAHAFLRALGRPA-----PQGF--MPSPTFD----- 145
DB 128 LYGVESKRRRERAGSMPSLTGCTPPREFKLIPLVFNENEKGRDFTGRKRKISGKII 187
OY 146 -----MAQL-----Y 150
DB 188 HKASVNMVHESKLVGFQOLCSNDTSDCATYTFSSGINAIQEMWYKLYHNYINAAOVLK 247
OY 151 ARAGSLDMLDLCRRFGOPCGPENFTTIFTRM-GKCYTFNSGADGAEITTTTRGMNG 209
DB 248 IMMSYSABEELVTCFFDGMSCARNFTELFHHPMYGNCITFNN-KENATITLSTSMGSEFG 306
OY 210 LIDMLDVOOEYLPVRWNEETPEFY--GIRVOIHSOEPIIDOLGVSFGYQTFVS 266
DB 307 LOVILYINDEY-----NPLVSSFGAKVLHQONEFYFIEDVGMEIFETAMSTIG 357
OY 267 COOQOLSLPRPWSGSSASLNPTEPEPSDPLGSPSP---SPPYTLMGRLACETRY 323
DB 358 MHLTSEFKLSEPYSCOTED-----GSDVPATNITYNAAVSLQICLYSCFOTK 403
OY 324 VARKGCGRNRY--MPGDVPCSPQOYKN---CAHPAIDILKRD---SCACPNPCASTRY 375
DB 404 MEKKGCGAQISPLRPANYCYQHHPNMICYQIYQAFVEELGCGSVCSQSSFKWM 463
OY 376 AKELSMVRIPSRAARFLA-----RKLRSEAYIAENVLADIFFEALNYETV 423
DB 464 TLTTSLAQPSEASEKWLNLVTDQSOQINKLKTID-----LAKLILFKDLNORSI 517
OY 424 EOKKAYESELIGDIGGOMGLFISGLTILEILDYLCVEPDKVLGYF----- 472
DB 518 MESPANSTIEMLLSNFGGOLGIMMSSVCVIEII---EVF---FLDFSIARROWHKA 570
OY 473 ---NRORSQRHSNTNLOEGLSHR---TQVPHLSLGRP-PPPPCAVYTTLSASHT 524
DB 571 KDMWARRQTPPETSPSSKRGODNALDTDDLPFTTSAMRLPAPAGSTVPGTPPPRINT 630
OY 525 CYL 527
DB 631 LRL 633

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RESULT 13
ID SCAA_RABIT STANDARD; PRT; 640 AA.
AC 097741;
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Amloride-sensitive sodium channel alpha-subunit (Epithelial Na+
DE channel alpha subunit) (Alpha ENac) (Nonvoltage-gated sodium channel
DE 1 alpha subunit) (SCN5A) (Alpha NaCh).
GN SCN5A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Kudacke O., Weisz E., Wiener H., Plass H.;
RT "The rabbit epithelial sodium channel.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC INHIBITED BY THE DIURETIC AMLORIDE. MEDIATES THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LONG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC SUBUNIT: HETEROETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO THE AMLORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
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CC -----
DR EMBL: AJ132108; CA010571.1; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 1.
DR PRINTS: PRO1078; AMINACHANNEL.
DR PROSITE: PS01206; ASC. 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 65 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 66 86 POTENTIAL.
FT DOMAIN 87 539 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 540 560 POTENTIAL.
FT DOMAIN 561 640 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 640 AA; 72734 MW; 17C84C100F69E133 CRC64;

Query Match 13.7%; Score 392; DB 1; Length 640;
Best Local Similarity 22.4%; Pred. No. 5.9e-24;
Matches 146; Conservative 95; Mismatches 252; Indels 158; Gaps 25;

OY 6 GPEE-ARRQPSD-----INVFASNSCMHGLGVFGGSLRLRGMAAAV 49
DB 12 GPETVAPQPTDEDEALIEFHRSYRELFOFCNNTTTHAIRKYCSKHNRMATAPAVLW 71
OY 50 VLSVATFLYQAEVRYVREHHQTALD-ERESHRLVFPVATTCINPLRRSRLTPN--- 105
DB 72 LCTFGMMYQFG--LLFGYFSYVNLNINLNSDKLVFPVAVTCVTLNRYRYEITDQKE 129

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